



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 166505

TO: Franco M Salvoza
Location: REM/3B49/3C18
Art Unit: 1648
Friday, September 23, 2005

Case Serial Number: 10/654737

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Salvoza,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527



STIC-Biotech/ChemLib

166505

From: Page, Thurman
Sent: Wednesday, September 21, 2005 4:08 PM
To: STIC-Biotech/ChemLib; Salvoza, Franco
Cc: Page, Thurman
Subject: FW: rush sequence search request

Importance: High

RUSH SEARCH APPROVED

-----Original Message-----

From: Salvoza, Franco
Sent: Wednesday, September 21, 2005 3:59 PM
To: Page, Thurman
Subject: rush sequence search request

Mr. Page,
I'd like to kindly request a rush sequence search for application 10/654,737. It is an overdue amendment which was transferred to me (a new junior examiner) from an examiner that has since left the USPTO.

I am interested in an updated search for SEQ ID NOs: 5 and 6 for this application as well as an interference search to prepare it for allowance.

thank you for your time and consideration.

best regards,

Franco Salvoza

Examiner Franco Salvoza
AU1648
REM 3B49
x8410

RECEIVED
SEP 21 2005
STIC/BIOTECH, DIV. 100
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 9/23
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 156.61 Seconds
(without alignments)
568.004 Million cell updates/sec

Title: US-10-654-737-5

Perfect score: 1172

Sequence: 1 MDPNTVSSFQVDCFLVHRK.....RPPLTPKQKRWARTIRSEV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1140	97.3	237	5 AAE23116	Influenza
2	1107	94.5	230	8 ADO14171	Influenza
3	1079	92.1	230	8 ADO14175	Influenza
4	1078	92.0	217	8 ADO14178	Influenza
5	1075	91.7	237	5 ABB05772	Influenza
6	1057	90.2	227	8 ADO14179	Influenza
7	1054	89.9	230	2 AA003522	Non-struc
8	1052	89.8	230	4 AA009027	Equine in
9	1050	89.6	230	4 AA009029	Equine in
10	1047	89.3	230	8 ADO14177	Influenza
11	1046	89.2	230	8 ADO14174	Influenza
12	1035	88.3	227	8 ADO14180	Influenza
13	1021	87.1	230	8 ADO14176	Influenza
14	1021	87.1	230	8 ADO14183	Influenza
15	1006	85.8	202	8 ADO14184	Influenza
16	844	72.0	230	8 ADO14181	Influenza
17	835	71.2	230	8 ADO14172	Influenza
18	813	69.4	173	8 ADO14173	Influenza
19	424	36.2	97	4 AA009028	Equine in
20	415.5	35.5	246	2 AA012714	Flu NS1-H
21	412	35.2	344	4 ABU71886	Human pro
22	411	35.1	124	8 ADO14182	Influenza
23	407.5	34.8	231	2 AAR20301	Val(1) to
24	406.5	34.7	309	2 AAR13175	NS1_81-RL
25	406.5	34.7	319	2 AAR07945	NS181RLFA

ALIGNMENTS

RESULT 1

AAE23116

ID AAE23116 standard; protein; 237 AA.

XX AC AAE23116;

XX DT 21-AUG-2002 (first entry)

XX DE Influenza A virus/singapore/1/57/ca NS1 mutant protein.

XX KW Attenuated influenza vaccine; prophylactic; therapeutic; infection; virucide; mutant; mutein; NS1 protein.

XX OS Influenza A virus.

XX OS Synthetic.

XX PN WO200224876-A2.

XX PD 28-MAR-2002.

XX PF 25-SEP-2001; 2001WO-EP011087.

XX PR 25-SEP-2000; 2000EP-00120896.

XX FA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX PI Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;

XX DR WPI; 2002-416282/44.

XX DR N-PSDB; AAD37061.

XX PT Manufacturing live vaccine, by infecting Vero cells with virus, combining cells with serum-free cell culture medium, incubating cells in presence of protease and nuclease, harvesting virus and preparing vaccine.

XX PS Example 4; Page 62-63; 90pp; English.

XX CC The present invention relates to a method for isolating viruses from various sources and for producing live attenuated influenza vaccines in a serum-free African Green monkey kidney (Vero) cell culture under conditions where alterations in the surface antigens of the virus due to adaptive selection are minimised or prevented. The method is useful for the manufacture of whole-virus vaccine, preferably attenuated live vaccine. It is useful for prophylactic or therapeutic administration against viral infection, preferably influenza virus infections. The present sequence is Influenza A virus/singapore/1/57/ca (cold adapted) NS1 mutant protein. This sequence is used in the exemplification of the invention

26 406.5 34.7 319 2 AAR13176
27 406.5 34.7 327 2 AAR13177
28 406.5 34.7 335 2 AAR13178
29 406 34.6 312 4 AAY72521
30 406 34.6 312 5 AAU74767
31 406 34.6 312 5 AAU74928
32 405.5 34.6 306 2 AAR38867
33 405.5 34.6 306 2 AAR60194
34 405 34.6 262 3 AAB26326
35 404 34.5 312 4 AAY72522
36 404 34.5 312 5 AAU74768
37 404 34.5 312 5 AAU74929
38 403.5 34.4 304 2 AAR60197
39 403.5 34.4 304 2 AAR60207
40 403.5 34.4 335 2 AAR13179
41 402.5 34.3 150 2 AAW35281
42 402.5 34.3 150 5 AAE16491
43 402.5 34.3 230 2 AAR38868
44 402.5 34.3 230 2 AAR60195
45 402.5 34.3 230 2 AAR60226

AAR13176 NS1_81-RL
AAR13177 NS1_81-RL
AAR13178 NS1_81-RL
AAY72521 NS1-P703P
AAU74767 Amino aci
AAU74928 Amino aci
AAR38867 Sequence
AAR60194 Immunogen
AAB26326 CASB618 p
AAY72522 NS1-P703P
AAU74768 Amino aci
AAU74929 Amino aci
AAR60197 Immunogen
AAR60207 Immunogen
AAR13179 NS1_81(NV
AAW35281 PorCine s
AAE16491 Influenza
AAR38868 Sequence
AAR60195 Immunogen
AAR60226 Immunogen

XX SQ Sequence 237 AA;
Query Match 97.3%; Score 1140; DB 5; Length 237;
Best Local Similarity 96.1%; Pred. No. 1.2e-118;
Matches 221; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGLNIETATRA 60
DB 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGLNIETATRV 60
QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMD 120
QY 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
DB 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSKV 230
RESULT 2
AD014171
ID AD014171 standard; protein; 230 AA.
XX AC AD014171;
XX DT 12-AUG-2004 (first entry)
XX DE Influenza A virus non-structural protein (NS)-1 #1.
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded-RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX OS Influenza A virus; A/Udorn/307/72 (H3N2).
XX PN WO2004043404-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036292.
XX PR 13-NOV-2002; 2002US-0425661P.
XX PT 10-JUN-2003; 2003US-0477453P.
XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX PI Montellione GT, Krug RM;
XX DR WPI; 2004-420083/39.
XX CC Identifying agents useful for treating influenza virus infection
CC comprises identifying compounds that inhibit binding between influenza
CC virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
CC the protein.
CC Disclosure; Page 11; 92pp; English.
CC This invention relates to a novel method of identifying an inhibitor of
CC influenza virus which comprises testing candidate compounds for their
CC ability to reduce the extent of binding between influenza virus non-
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
CC domain and a dsRNA that binds the protein. The invention may be useful
CC for the production of compounds with a virucide activity acting as
CC inhibitors of binding between influenza virus non-structural protein-1
CC (NS1) and double-stranded RNA. It is possible that binding of double-
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA

CC -activated protein kinase to remain in an inactive state so that it does
CC not catalyze the phosphorylation of translation inhibition factor
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
CC replication. The invention is useful as a (high throughput) screening
CC method for identifying compounds having inhibitory activity against
CC influenza virus. Compounds identified are useful in treating animals,
CC including human infected with influenza virus. The present sequence is
CC that of an influenza virus non-structural (NS)-1 protein which is related
CC to the method of the invention.
SQ Sequence 230 AA;
Query Match 94.5%; Score 1107; DB 8; Length 230;
Best Local Similarity 93.5%; Pred. No. 5.9e-115;
Matches 215; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGLNIETATRA 60
DB 1 MDPNTVSSFOVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGLDIETATRA 60
QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMD 120
QY 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTAEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
DB 181 LIGGLEWNNNTVRVSETLQRFARWSSNENGRPPLTPKQKRWAGTIRSEV 230
RESULT 3
AD014175
ID AD014175 standard; protein; 230 AA.
XX AC AD014175;
XX DT 12-AUG-2004 (first entry)
XX DE Influenza A virus non-structural protein (NS)-1 #5.
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded-RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX OS Influenza A virus.
XX PN WO2004043404-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036292.
XX PR 13-NOV-2002; 2002US-0425661P.
XX PT 10-JUN-2003; 2003US-0477453P.
XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX PI Montellione GT, Krug RM;
XX DR WPI; 2004-420083/39.
XX CC Identifying agents useful for treating influenza virus infection
CC comprises identifying compounds that inhibit binding between influenza
CC virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
CC the protein.
CC Disclosure; Page 12; 92pp; English.
XX

XX (AMCY) AMERICAN CYANAMID CO.
 XX Galarza JM, Latham TE;
 XX WPI; 2002-139923/18.
 XX N-PSDB; ABA93942.
 XX Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
 XX polypeptide, useful in diagnosis and for generating new influenza A
 XX variant strains.
 XX Disclosure; Page 78-79; 103pp; English.
 XX The present invention describes an isolated polynucleotide (I) having the
 XX complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
 XX strand, antigenomic message sense. ABA93934 to ABA93944 encode the
 XX Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05774
 XX from the present invention. (I) is useful for designing polymerase chain
 XX reaction (PCR) primers for use in a PCR assay to detect the presence of
 XX the corresponding virus segment in a sample or for designing and
 XX selecting peptides for use in an enzyme linked immunosorbent assay to
 XX detect the presence of the corresponding protein produced by that segment
 XX in a sample, hence is useful in diagnosis and may be modified by mutation
 XX to generate new influenza A variant strains. ABA94945 to ABA94939
 XX represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
 XX are used in an example from the present invention
 XX Sequence 237 AA;
 XX Query Match 91.7%; Score 1075; DB 5; Length 237;
 XX Best Local Similarity 90.4%; Pred. No. 2.3e-111;
 XX Matches 208; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 MDNPTVSSFOVDCFLMHWKRVKADQELGDAPFLDLRRDQKSLRGSTGLNIETAIRA 60
 Db 1 MDSNTVSSFOVDCFLMHWKRVKADQELGDAPFLDLRRDQKSLRGSTGLNIETATHV 60
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWFMLMPKQKVGPLCIRMD 120
 Db 61 GKQIVEKILKEESDEALKMTWASTPASYITDMTIEELSRDWFMLMPKQKVGPLCIRID 120
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Db 121 QAIMDKNIMLKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTIEDYKNAIGV 180
 Qy 181 LIGGLEWNNNTVRVSKTLORFAWSSNENGRPPLTPKQKQKARTIRSEV 230
 Db 181 LIGGLEWNNNTVRVSKTLORFAWSSNENGRPPLTPKQKQKARTARSKV 230
 RESULT 6
 AD014179
 ID AD014179 standard; protein; 227 AA.
 XX AC
 XX AD014179;
 XX 12-AUG-2004 (first entry)
 XX Influenza A virus non-structural protein (NS)-1 #9.
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 XX double-stranded RNA; dsRNA; binding domain; virucide;
 XX double-stranded-RNA-activated protein kinase; phosphorylation;
 XX translation inhibition factor; eIF2alpha; viral protein synthesis;
 XX viral protein replication; screening method; infection.
 XX Influenza A virus.
 XX OS
 XX WO2004043404-A2.
 XX 27-MAY-2004.
 XX

PF 13-NOV-2003; 2003WO-US036292.
 XX 13-NOV-2002; 2002US-0425661P.
 PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX Montellione GT, Krug RM;
 XX WPI; 2004-420083/39.
 XX Identifying agents useful for treating influenza virus infection
 XX comprises identifying compounds that inhibit binding between influenza
 XX virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 XX the protein.
 XX Disclosure; Page 13; 92pp; English.
 XX This invention relates to a novel method of identifying an inhibitor of
 XX influenza virus which comprises testing candidate compounds for their
 XX ability to reduce the extent of binding between influenza virus non-
 XX structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 XX domain and a dsRNA that binds the protein. The invention may be useful
 XX for the production of compounds with a virucide activity acting as
 XX inhibitors of binding between influenza virus non-structural protein-1
 XX (NS1) and double-stranded RNA. It is possible that binding of double-
 XX stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 XX -activated protein kinase to remain in an inactive state so that it does
 XX not catalyse the phosphorylation of translation inhibition factor and
 XX eIF2alpha, which would otherwise inhibit viral protein synthesis and
 XX replication. The invention is useful as a (high throughput) screening
 XX method for identifying compounds having inhibitory activity against
 XX influenza virus. Compounds identified are useful in treating animals,
 XX including human infected with influenza virus. The present sequence is
 XX that of an influenza virus non-structural (NS)-1 protein which is related
 XX to the method of the invention.
 XX Sequence 227 AA;
 XX Query Match 90.2%; Score 1057; DB 8; Length 227;
 XX Best Local Similarity 90.7%; Pred. No. 2.3e-109;
 XX Matches 206; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 Qy 4 NTVSSFOVDCFLMHWKRVKADQELGDAPFLDLRRDQKSLRGSTGLNIETAIRACKQ 63
 Db 1 NTVSSFOVDCFLMHWLKRFDQELGDAPFLDLRRDQKSLRGSTGLDIETATRACKQ 60
 Qy 64 IVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWFMLMPKQKVGPLCIRMDQAI 123
 Db 61 IVERILKEESDEALKMNIASVPASRYLTDMTIEMSRDWFMLMPKQKVGSLCIRMDQAI 120
 Qy 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183
 Db 121 MDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTDEDVKNAIGLIG 180
 Qy 184 GLEWNNNTVRVSKTLORFAWSSNENGRPPLTPKQKQKARTIRSEV 230
 Db 181 GLEWNNNTVRVSKTLORFAWSSNENGRPPLPPKQKQKARTIRSEV 227
 RESULT 7
 AA003522
 ID AA003522 standard; protein; 230 AA.
 XX AC
 XX AA003522;
 XX 16-OCT-2003 (revised)
 DT 09-APR-1997 (first entry)
 XX Non-structural protein NS1 of influenza A virus.
 XX Non-structural protein; NS1; influenza virus; respiratory tract;
 XX diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify.
 XX

XX OS Influenza virus; A/equine 1/Suffolk 89.
 XX PN BP726316-A2.
 XX PN 14-AUG-1996.
 XX PD 31-JAN-1996; 96EP-00300681.
 XX PR 09-FEB-1995; 95GB-00002489.
 XX PA (ANIM-) ANIMAL HEALTH TRUST.
 XX PI Binns M, Birch-Machin I;
 XX WPI; 1996-364394/37.
 DR N-PSDB; AAT37435.
 XX Recombinant equine influenza virus NS1 protein - useful for diagnosis of
 PT equine influenza A.
 PS Example; Fig 1A; 20pp; English.
 XX This sequence represents non-structural protein NS1 of influenza virus
 CC A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine
 CC influenza A infections by detection of anti-NS1 antibodies. The NS1
 CC coding sequence was isolated using the primer sequences given in AAT37436
 CC -40. (Updated on 16-OCT-2003 to standardise OS field)
 XX SQ Sequence 230 AA;

Query Match 89.94; Score 1054; DB 2; Length 230;
 Best Local Similarity 88.3%; Pred. No. 5e-109;
 Matches 203; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLNLTETAIRA 60
 Db 1 MDSNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLDLETATRA 60
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 120
 Db 61 GKQIVEQILEESDEAFQMTIASVPASRYLTDMTLDEMSTRDWFMLMPKQKVAGPLCIRMD 120
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Db 121 QAIMDKNIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNIGV 180
 Qy 181 LIGGLENNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIESEV 230
 Db 181 LIGGLKWNNDTVRVSSETLQRFARWSSHENGSRPSFPKQKRMERTIESEV 230

RESULT 8
 AAE09027
 ID AAE09027 standard; protein; 230 AA.
 AC AAE09027;
 XX 15-NOV-2001 (first entry)
 XX Equine influenza virus H3N8 Peiwt1NS230 protein.
 XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 XX vaccine; neiwt1NS891 DNA; Peiwt1NS230 protein.
 XX Equine influenza virus H3N8.
 XX WO200160849-A2.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005048.
 XX

PR 16-FEB-2000; 2000US-00506286.
 XX (UYPI-) UNIV PITTSBURGH.
 XX Dowling PW, Youngner JS;
 XX WPI; 2001-522584/57.
 DR N-PSDB; AAD15678.
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 PT proteins and viruses containing nucleic acid molecules encoding the
 PT proteins, which are useful for protecting animals from influenza virus
 PT infections.
 XX Claim 5; Page 72-73; 172pp; English.
 XX The patent discloses cold-adapted equine influenza viruses and
 CC reassortant influenza A viruses comprising at least one genome segment of
 CC such an equine influenza virus, wherein the equine influenza virus genome
 CC segment confers at least one identifying phenotype of the cold-adapted
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,
 CC dominant interference or attenuation. The viruses are useful for
 CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is an equine influenza (ei)
 CC virus H3N8 Peiwt1 (wild type) NS230 protein which is encoded by
 CC neiwt1NS891 DNA
 XX SQ Sequence 230 AA;

Query Match 89.8%; Score 1052; DB 4; Length 230;
 Best Local Similarity 87.8%; Pred. No. 8.4e-109;
 Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLNLTETAIRA 60
 Db 1 MDSNTVSSFOVDCFLMHWVRKRVADQELGDAPFLDLRRDQKSLGRGSLGLDLETATRA 60
 Qy 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWFMLMPKQKVAGPLCIRMD 120
 Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSTRDWFMLMPKQKVAGPLCIRMD 120
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Db 121 QAIMDKNIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNIGV 180
 Qy 181 LIGGLENNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRMARTIESEV 230
 Db 181 LIGGLKWNNDTVRVSSETLQRFARWSSHENGSRPSFPKQKRMERTIESEV 230

RESULT 9
 AAE09029
 ID AAE09029 standard; protein; 230 AA.
 AC AAE09029;
 XX 15-NOV-2001 (first entry)
 XX Equine influenza virus H3N8 Peiwt1NS230 protein.
 XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 XX vaccine; neiwt1NS891 DNA; Peiwt1NS230 protein.
 XX Equine influenza virus H3N8.
 XX WO200160849-A2.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005048.
 XX 16-FEB-2000; 2000US-00506286.
 XX

PA (UYFI-) UNIV PITTSBURGH.
 PI Dowling PW, Youngner JS;
 XX WPI; 2001-522584/57.
 DR N-PSDB; AAD15681.
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 PT proteins and viruses containing nucleic acid molecules encoding the
 PT proteins, which are useful for protecting animals from influenza virus
 PT infections.
 XX Claim 5; Page 77; 172pp; English.
 PS The patent discloses cold-adapted equine influenza viruses and
 XX reassortant influenza A viruses comprising at least one genome segment of
 CC such an equine influenza virus, wherein the equine influenza virus genome
 CC segment confers at least one identifying phenotype of the cold-adapted
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,
 CC dominant interference or attenuation. The viruses are useful for
 CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is equine influenza (ei)
 CC virus H3N8 Peical (cold adapted) NS230 protein which is encoded by
 CC neicalNS888 DNA
 XX Sequence 230 AA;
 PS Query Match 89.8%; Score 1052; DB 4; Length 230;
 XX Best Local Similarity 87.8%; Pred. No. 8.4e-109; Indels 0; Gaps 0;
 CC Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNETAIRA 60
 DB 1 MDSNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNETAIRA 60
 QY 61 GKQIVRLKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCTIRMD 120
 DB 61 GKQIVRLKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCTIRMD 120
 QY 121 QAIMDKSILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 QY 181 LIGGLENNNTVRVSKTQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
 DB 181 LIGGLKNDNTVRISETLQRFARWSSHENGSRPFPKQKRMWERTISPEV 230
 RESULT 10
 ID ADO14177 standard; protein; 227 AA.
 XX AC ADO14177;
 XX DT 12-AUG-2004 (first entry)
 XX DE Influenza A virus non-structural protein (NS)-1 #7.
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 KW double-stranded RNA; dsRNA; binding domain; virucide;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;
 KW viral protein replication; screening method; infection.
 XX Influenza A virus.
 OS WO2004043404-A2.
 XX PN 27-MAY-2004.
 XX PD 13-NOV-2003; 2003WO-US036292.
 XX PF 13-NOV-2002; 2002US-0425661P.
 XX PR

PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA Montelione GT, Krug RM;
 XX WPI; 2004-420083/39.
 DR Identifying agents useful for treating influenza virus infection
 XX comprises identifying compounds that inhibit binding between influenza
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 PT the protein.
 XX Disclosure; Page 13; 92pp; English.
 PS This invention relates to a novel method of identifying an inhibitor of
 XX influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding between influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC -activated protein kinase to remain in an inactive state so that it does
 CC not catalyze the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.
 XX Sequence 227 AA;
 PS Query Match 89.8%; Score 1050; DB 8; Length 227;
 XX Best Local Similarity 91.2%; Pred. No. 1.4e-108; Indels 0; Gaps 0;
 CC Matches 207; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 4 NTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNETAIRAGKQ 63
 DB 1 NTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSTGLGNETAIRAGKQ 60
 QY 64 IVERILKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCTIRMDQAI 123
 DB 61 IVERILVEESDEALKMTIVSMPASRYLTDMTIEMSRDWFMMPKQVAGSLCIRMDQAI 120
 QY 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183
 DB 121 MDKNIILKANFSVISRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGDLIG 180
 QY 184 GLEWNNNTVRVSKTQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
 DB 181 GLEWNNNTVRVSKTQRFARWSSNENGRPPLTPKQKRMARTIRSEV 227
 RESULT 11
 ID ADO14174 standard; protein; 230 AA.
 XX AC ADO14174;
 XX DT 12-AUG-2004 (first entry)
 XX DE Influenza A virus non-structural protein (NS)-1 #4.
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 KW double-stranded RNA; dsRNA; binding domain; virucide;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;
 KW viral protein replication; screening method; infection.
 XX

OS Influenza A virus.
 PN WO2004043404-A2.
 XX 27-MAY-2004.
 XX 13-NOV-2003; 2003WO-US036292.
 XX 13-NOV-2003; 2002US-0425661P.
 PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA Montellione GT, Krug RM;
 XX WPI; 2004-420083/39.
 XX Identifying agents useful for treating influenza virus infection
 PT comprises identifying compounds that inhibit binding between influenza
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 PT the protein.
 XX Disclosure; Page 12; 92pp; English.
 PS This invention relates to a novel method of identifying an inhibitor of
 CC influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding between influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC activated protein kinase to remain in an inactive state so that it does
 CC not catalyze the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.
 XX Sequence 230 AA;
 SQ
 Query Match 89.3%; Score 1047; DB 8; Length 230;
 Best Local Similarity 88.7%; Pred. No. 3e-108;
 Matches 204; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFQVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGNIETATRA 60
 DB 1 MDSNTVSSFQVDCFLHVRKRVADQEMGDAPFLDLRLRDQKSLRGSGTLGDIETATRA 60
 QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMD 120
 DB 61 GKQIVERILEESDEALKMTIASAPSVRYLPDMTLEMSRDWFMMPKQKVGSLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLSPGHTNEDIKNAIGV 180
 DB 121 QAIMDKNITLKANFSIIIFDRLETLILLRAFTEEGAIVGEISVPVSLPGHTDEDVKNIGV 180
 QY 181 LIGGLEWNNNTVRSVKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWNDNTVRDSETLQRFAPWSSNEDRRPPLPKQKRWARTIESEV 230
 RESULT 12
 ID ADO14180
 ID ADO14180 standard; protein; 227 AA.
 XX ADO14180;
 AC
 XX 12-AUG-2004 (first entry)
 DT

XX Influenza A virus non-structural protein (NS)-1 #10.
 DE influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 XX double-stranded RNA; dsRNA; binding domain; virucide;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;
 KW viral protein replication; screening method; infection.
 XX Influenza A virus.
 OS WO2004043404-A2.
 XX 27-MAY-2004.
 XX 13-NOV-2003; 2003WO-US036292.
 XX 13-NOV-2003; 2002US-0425661P.
 PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA Montellione GT, Krug RM;
 XX WPI; 2004-420083/39.
 XX Identifying agents useful for treating influenza virus infection
 PT comprises identifying compounds that inhibit binding between influenza
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 PT the protein.
 XX Disclosure; Page 13-14; 92pp; English.
 PS This invention relates to a novel method of identifying an inhibitor of
 CC influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding between influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC activated protein kinase to remain in an inactive state so that it does
 CC not catalyze the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.
 XX Sequence 227 AA;
 SQ
 Query Match 89.2%; Score 1046; DB 8; Length 227;
 Best Local Similarity 90.7%; Pred. No. 3.9e-108;
 Matches 206; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 4 NTVSSFQVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGNIETATRAKQ 63
 DB 1 NTVSSFQVDCFLHVRKRVADQELGDPFLDLRLRDQKSLRGSGTLGDIETATRAKQ 60
 QY 64 IVERILKEESDEALKMTWASAPASRYLTDMTTEMSRDWFMMPKQKVGAPLCIRMDQAI 123
 DB 61 IVERILEESDETLKMTIASAPAFRYPTDMTLEMSRDWFMMPKQKVGSLCIRMDQAI 120
 QY 124 MDKSIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLSPGHTNEDIKNAIGV 183
 DB 121 MDKNIILKANFSVIFDRLETLILLRAFTEEGAIVGEISPLSPGHTNEDVKNIGV 180
 QY 184 GLEWNNNTVRSVKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 GLEWNDNTVRVSETLQRFAPWSSNENGRPPLTPKQKRWARTIESEV 227

Best Local Similarity 85.7%; Pred. No. 2.5e-105;
Matches 197; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETAIRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRE 60

Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCIRMD 120
Db 61 GKHIVERILEESDEALKMTIASVPASRYLTEMTELEMSRDWMLIPKQKVTGPGLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Db 121 QAVGKTIILKANFSVIFNRLEALILRAFTDEGAIVGEISPLSPGHTNEDVKNAGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPAWSSNENGRPPLTPKQKQWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSETLQRFWRSSDENGRSPLPPKQKQKVERTIEPEV 230

RESULT 15
ADO14184
ID ADO14184 standard; protein; 202 AA.
XX AC ADO14184;
XX DT 12-AUG-2004 (first entry)
XX DE Influenza A virus non-structural protein (NS)-1 #14.
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded-RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX OS Influenza A virus; STRAIN A/FORT MONMOUTH/1/47.
XX PN WO2004043404-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036292.
XX PR 13-NOV-2003; 2002US-0425661P.
XX PR 10-JUN-2003; 2003US-0477453P.
XX PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX PI Montelione GT, Krug RM;
XX DR WPI; 2004-420083/39.
XX PT Identifying agents useful for treating influenza virus infection
PT comprises identifying compounds that inhibit binding between influenza
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
PT the protein.
XX PS Disclosure; Page 14; 92pp; English.
XX CC This invention relates to a novel method of identifying an inhibitor of
CC influenza virus which comprises testing candidate compounds for their
CC ability to reduce the extent of binding between influenza virus non-
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
CC domain and a dsRNA that binds the protein. The invention may be useful
CC for the production of compounds with a virucide activity acting as
CC inhibitors of binding between influenza virus non-structural protein-1
CC (NS1) and double-stranded RNA. It is possible that binding of double-
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
CC -activated protein kinase to remain in an inactive state so that it does
CC not catalyse the phosphorylation of translation inhibition factor and
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
CC replication. The invention is useful as a (high throughput) screening

CC method for identifying compounds having inhibitory activity against
CC influenza virus. Compounds identified are useful in treating animals,
CC including human infected with influenza virus. The present sequence is
CC that of an influenza virus non-structural (NS)-1 protein which is related
CC to the method of the invention.
SQ Sequence 202 AA;

Query Match 85.8%; Score 1006; DB 8; Length 202;
Best Local Similarity 97.5%; Pred. No. 9.8e-104;
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETAIRA 60
Db 1 MDPNTVSSFOVDCFLMHWKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRV 60

Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEMSRDWFMMPKQVAGPLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
Db 121 QAIMDKSIILKANFSVIFDRLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPAWSSNENGRPPLTPKQKQWARTIRSEV 202
Db 181 LIGGLEWNNNTVRVSKTLQRFAPAWSSNENGRPPLTPKQKQKVERTIEPEV 202

Search completed: September 22, 2005, 21:42:21
Job time : 159.61 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1142	97.4	237	1	MNV177	nonstructural prot
2	1140	97.3	237	1	MNV174	nonstructural prot
3	1128	96.2	237	1	MNV1C1	nonstructural prot
4	1111	94.8	230	1	MNV1V1	nonstructural prot
5	1107	94.5	230	2	S03648	nonstructural prot
6	1092	93.2	230	1	MNV1A2	nonstructural prot
7	1079	92.1	230	1	MNV1A3	nonstructural prot
8	1078	92.0	217	1	MNV1V61	nonstructural prot
9	1075	91.7	230	1	MNV1V4	nonstructural prot
10	1075	91.7	237	1	MNV1V1A	nonstructural prot
11	1061	90.5	227	1	MNV1X3	nonstructural prot
12	1057	90.2	227	1	MNV1X9	nonstructural prot
13	1057	90.2	230	1	MNV1V1F	nonstructural prot
14	1055	90.0	230	1	MNV1V1	nonstructural prot
15	1050	89.6	227	1	MNV1X5	nonstructural prot
16	1050	89.6	237	1	MNV1V1K	nonstructural prot
17	1049	89.5	227	1	MNV1XV7	nonstructural prot
18	1046	89.2	227	1	MNV1XV1	nonstructural prot
19	1029	87.8	230	1	D45539	nonstructural prot
20	999	85.2	202	1	MNV1V47	nonstructural prot
21	844	72.0	230	1	MNV1V16	nonstructural prot
22	840	71.7	230	1	MNV1V45	nonstructural prot
23	840	71.7	230	1	MNV1V46	nonstructural prot
24	838	71.5	230	1	MNV1V48	nonstructural prot
25	837	71.4	230	1	MNV1V47	nonstructural prot
26	824	70.3	230	2	A45575	nonstructural prot
27	437	37.3	89	2	B92982	nonstructural prot
28	411	35.1	124	1	MNV1V71	nonstructural prot
29	151	12.9	32	2	PQ0419	nonstructural prot

A:Residues: 1-237 <KRY>
 A:Cross-references: GB:K00576; NID:G324813; PIDN:AAA43525.1; PID:G324815
 C:Genetics:
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing

Query Match 97.3%; Score 1140; DB 1; Length 237;
 Best Local Similarity 96.5%; Pred. No. 4.6e-91;
 Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRV 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDVKNAGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWSDNTVRVSKTLQRFAMRSSSENENGRPPLTPKQKRWARTIRSEV 230

RESULT 3
 MNIVCI
 nonstructural protein NS1 - influenza A virus (strain A/Chile/1/83 [H1N1])
 C:Species: influenza A virus
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 07-Jun-1996
 C:Accession: A34215; S04836
 R:Schreier, E.; Roeseke, H.; Michel, S.
 Nucleic Acids Res. 17, 5381, 1989
 A:Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1).
 A:Reference number: A34215; MUID:89345097; PMID:2762132
 A:Accession: A34215
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-237 <SCH>
 A:Cross-references: EMBL:X15282
 C:Genetics:
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing; nonstructural protein

Query Match 96.2%; Score 1128; DB 1; Length 237;
 Best Local Similarity 95.2%; Pred. No. 5e-90;
 Matches 219; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGDIETATCV 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCVRMD 120
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDVKNAGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWSDNTVRVSKTLQRFAMRSSSENENGRPPLTPKQKRWARTIRSEV 230

RESULT 4
 MNIV1
 nonstructural protein NS1 - influenza A virus (strain A/PR/8/34)
 C:Species: influenza A virus

C:Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 30-Sep-1993
 C:Accession: A04089
 R:Baer, M.; Taussig, R.; Zakra, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.
 Nucleic Acids Res. 8, 5845-5858, 1980
 A:Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and compa
 A:Reference number: A93714; MUID:81124304; PMID:7465426
 A:Accession: A04089
 A:Molecule type: genomic RNA
 A:Residues: 1-230 <BAE>
 C:Genetics:
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing

Query Match 94.8%; Score 1111; DB 1; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.4e-88;
 Matches 216; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGLDIETATRA 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASVPASRYLTDMTTEEMSRDWSMLIPKQKVAGPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTAEIDVKNAGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWSDNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230

RESULT 5

S09648
 nonstructural protein NS1 - influenza A virus (strain A/Leningrad/1/54)
 C:Species: influenza A virus
 C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 19-May-2000
 C:Accession: S09648
 R:Beklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mamae
 Bioorg. Khim. 11, 641-645, 1985
 A:Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 of
 A:Reference number: S09648; MUID:85307107; PMID:4038350
 A:Accession: S09648
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-230 <BBK>
 A:Cross-references: EMBL:X52146; NID:G60716; PIDN:CAA36392.1; PID:G60717
 C:Superfamily: influenza virus nonstructural protein NS1

Query Match 94.5%; Score 1107; DB 2; Length 230;
 Best Local Similarity 93.5%; Pred. No. 3.1e-88;
 Matches 215; Conservative 10; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRRDQKSLRGSGTLGLDIKTATRA 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASVPASRYLTDMTTEEMSRDWSMLIPKQKVAGPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTNEIDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLPSLPGLTAEIDVKNAGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWSDNTVRVSKTLQRFAMRSSNENGRPPLTPKQKRWARTIRSEV 230

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RESULT 6
MNIV2
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6750/78)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:Cross-references: UNIPROT:P13138
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.2%; Score 1092; DB 1; Length 230;
Best Local Similarity 92.6%; Pred. No. 6.2e-87;
Matches 213; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGDIETATRA 60

Qy 61 GQIVVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVGAPLCIRMD 120
Db 61 GQIVVERILEESDEALKMTIASVPASRYLTDMTIEEMSRDWMFLMPKQKVGAGSLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAINDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPPKQKRWARTISEV 230
Db 181 LIGGLEWNDNTVRVSETLQRFAPWSSNENGRPPLTPPKQKRWARTIESEV 230

RESULT 7
MNIV3
nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6874/78)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: E32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: E32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:Cross-references: UNIPROT:P13139
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.1%; Score 1079; DB 1; Length 230;
Best Local Similarity 91.7%; Pred. No. 8.2e-86;
Matches 211; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDSNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGDIETATRA 60

Qy 61 GQIVVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVGAPLCIRMD 120
Db 61 GQIVVERILEESDEALKMTIASVPASRYLTDMTIEEMSRDWMFLMPKQKVGAGSLCIRMD 120
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Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAINDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPPKQKRWARTISEV 230
Db 181 LIGGLEWNDNTVRVSETLQRFAPWSSNENGRPPLTPPKQKRWARTIESEV 230

RESULT 8
MNIV61
nonstructural protein NS1 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])
C:Species: influenza A virus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: G31831
R:Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeye, C.
Virology 167, 554-567, 1988
A:Title: Identification of sequence changes in the cold-adapted, live attenuated influen:
A:Reference number: A31831; MUID:89073759; PMID:2974219
A:Accession: G31831
A:Molecule type: genomic RNA
A:Residues: 1-217 <CO>
A:Cross-references: GB:M23968; GB:J04349; GB:M23969; NID:G324860; PIDN:AAA43553.1; PID:9;
C:Genetics:
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.0%; Score 1078; DB 1; Length 217;
Best Local Similarity 96.3%; Pred. No. 9.3e-86;
Matches 209; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGNIETATRA 60
Db 1 MDPNTVSSFOVDCFLHVRKRVADQELGDAPEFLDLRLRDQSLRGSGTLGNIETATRV 60

Qy 61 GQIVVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVGAPLCIRMD 120
Db 61 GQIVVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVGAPLCIRMD 120

Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
Db 121 QAINDKNIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPSLPGHTDVEDVNAIGV 180

Qy 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPK 217
Db 181 LIGGLEWNDNTVRVSKTLQRFAPWSSNENGRPPLTPK 217

RESULT 9
MNIV44
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, a
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TR>
A:Cross-references: UNIPROT:P13140
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 91.7%; Score 1075; DB 1; Length 230;
Best Local Similarity 91.3%; Pred. No. 1.8e-85;
Matches 210; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
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Qy 1 MDPNTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
 Db 1 MDSNTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
 Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMD 120
 Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMD 120
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Qy 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
 Db 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230

RESULT 10
 MNVIA
 nonstructural protein NS1 - influenza A virus (strain A/Udm/72 [H3N2])
 C:Species: influenza A virus
 C:Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
 C:Accession: A04088; S11297
 R:Lamb, R.A.; Lai, C.J.
 Cell 21, 475-485, 1980
 A:Title: Sequence of interrupted and uninterrupted mRNAs and cloned DNA coding for the
 A:Reference number: A90801; MUID:81001890; PMID:7407920
 A:Accession: A04088
 A:Molecule type: mRNA
 A:Residues: 1-237 <NAK>
 A:Cross-references: UNIPROT:P03495; GB:V01102; GB:J02169; NID:660797; PIDN:CAA24288.1; F
 A:Experimental source: strain A/Udm/72 [H3N2]
 R:Robertson, J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza
 A:Reference number: S11286; MUID:80034428; PMID:493121
 A:Accession: S11297
 A:Molecule type: Genomic RNA
 A:Residues: 1-15 <ROB>
 A:Cross-references: GB:J02118
 A:Experimental source: strain A/Fpv/Rostock/34 [H7N1]
 A:Note: the authors translated the codon CAG for residue 10 as Glu
 C:Genetics:
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing

Query Match 91.7%; Score 1075; DB 1; Length 237;
 Best Local Similarity 90.4%; Pred. No. 1.9e-85;
 Matches 208; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
 Db 1 MDSNTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
 Qy 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMD 120
 Db 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMD 120
 Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGV 180
 Qy 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
 Db 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230

RESULT 11
 MNVIX3
 nonstructural protein NS1 - influenza A virus (strain A/Duck/England/56 [H1N6]) (fragme
 C:Species: influenza A virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C:Accession: C27846
 R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
 Virology 158, 465-469, 1987
 A:Title: Genetic divergence of the NS genes of avian influenza viruses.
 A:Reference number: A94361; MUID:87236215; PMID:2954302
 C:Accession: C27846
 A:Molecule type: genomic RNA
 A:Residues: 1-227 <NAK>
 A:Cross-references: GB:M16563; NID:G324786; PIDN:AAA43510.1; PID:G324787
 C:Genetics:
 A:Gene: NS1
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing; nonstructural protein

Query Match 90.5%; Score 1061; DB 1; Length 227;
 Best Local Similarity 91.2%; Pred. No. 2.9e-84;
 Matches 207; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 4 NTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRACKQ 63
 Db 1 NTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRACKQ 60
 Qy 64 IVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMDQAI 123
 Db 61 IVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMDQAI 120
 Qy 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183
 Db 121 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 180
 Qy 184 GLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
 Db 181 GLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 227

RESULT 12
 MNVIX9
 nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fre
 C:Species: influenza A virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
 C:Accession: I27846
 R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
 Virology 158, 465-469, 1987
 A:Title: Genetic divergence of the NS genes of avian influenza viruses.
 A:Reference number: A94361; MUID:87236215; PMID:2954302
 C:Accession: I27846
 A:Molecule type: genomic RNA
 A:Residues: 1-227 <NAK>
 A:Cross-references: GB:M17070; NID:G324854; PIDN:AAA43548.1; PID:G324855
 C:Genetics:
 A:Gene: NS1
 A:Map position: segment 8
 C:Superfamily: influenza virus nonstructural protein NS1
 C:Keywords: alternative splicing; nonstructural protein

Query Match 90.2%; Score 1057; DB 1; Length 227;
 Best Local Similarity 90.7%; Pred. No. 6.4e-84;
 Matches 206; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 4 NTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRACKQ 63
 Db 1 NTVSSFOVDCFLWHVVRKRVADQELGDPAPFLDLRLRDQKSLRGSTGLGNIETAIRACKQ 60
 Qy 64 IVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMDQAI 123
 Db 61 IVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWFMLMPKQKQVAGPLCIRMDQAI 120
 Qy 124 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 183
 Db 121 MDKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLSPGHTNEDIKNAIGVLIG 180
 Qy 184 GLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:32:32 ; Search time 143.504 Seconds
(without alignments)
820.730 Million cell updates/sec

Title: US-10-654-737-5
Perfect score: 1172
Sequence: 1 MDPNTVSSFQVDCFLHVRK.....RPPLTPKQKRWARTIRSEV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1143	97.5	237	2 Q6XTI8	Q6xti8 influenza a
2	1142	97.4	237	1 VNS1_IATUSS	P03498 influenza a
3	1142	97.4	237	2 Q6XTI4	Q6xti4 influenza a
4	1142	97.4	237	2 Q6XTI6	Q6xti6 influenza a
5	1142	97.4	237	2 Q6XTJ6	Q6xtj6 influenza a
6	1141	97.4	230	1 VNS1_TALE1	P26131 influenza a
7	1141	97.4	237	2 Q6XTJ2	Q6xtj2 influenza a
8	1140	97.3	237	1 VNS1_IATOW	P03497 influenza a
9	1139	97.2	237	2 Q6XTJ4	Q6xtj4 influenza a
10	1138	97.1	237	2 Q6XTJ8	Q6xtj8 influenza a
11	1129	96.3	230	2 Q6XTI2	Q6xti2 influenza a
12	1128	96.2	237	1 VNS1_TACHI	P11618 influenza a
13	1125	96.0	237	2 Q6XTJ0	Q6xtj0 influenza a
14	1124	95.9	230	2 Q82505	Q82505 influenza a
15	1123	95.8	233	2 Q84068	Q84068 influenza a
16	1118	95.4	230	2 Q82506	Q82506 influenza a
17	1116	95.2	230	2 Q67249	Q67249 influenza a
18	1116	95.2	237	2 Q6XTH0	Q6xth0 influenza a
19	1116	95.2	237	2 Q6XTH2	Q6xth2 influenza a
20	1116	95.2	237	2 Q6XTH6	Q6xth6 influenza a
21	1116	95.2	237	2 Q6XTH8	Q6xth8 influenza a
22	1116	95.2	237	2 Q6XTI0	Q6xti0 influenza a
23	1113	95.0	237	2 Q6XTH4	Q6xth4 influenza a
24	1111	94.8	230	1 VNS1_IAPUE	P03496 influenza a
25	1111	94.8	230	2 Q71QT3	Q71qt3 influenza a
26	1110	94.7	237	2 Q6XTG8	Q6xtg8 influenza a
27	1110	94.7	237	2 Q9DUT8	Q9dut8 influenza a
28	1107	94.5	230	1 VNS1_IALEN	P17042 influenza a
29	1107	94.5	230	2 Q67267	Q67267 influenza a
30	1107	94.5	230	2 Q6LD08	Q6ld08 influenza a
31	1107	94.5	230	2 Q76MT8	Q76mt8 influenza a

32	1105	94.3	237	2 Q6XTC4	Q6xtc4 influenza a
33	1105	94.3	237	2 Q6XTE2	Q6xtc2 influenza a
34	1105	94.3	237	2 Q6XTE4	Q6xtc4 influenza a
35	1105	94.3	237	2 Q6XTE6	Q6xtc6 influenza a
36	1104	94.2	237	2 Q6XTG4	Q6xtg4 influenza a
37	1103	94.1	230	2 Q99AU3	Q99au3 influenza a
38	1103	94.1	237	2 Q6XTP6	Q6xtf6 influenza a
39	1102	94.0	230	2 OS7272	OS7272 influenza a
40	1101	93.9	237	2 Q91OP3	Q91op3 influenza a
41	1101	93.9	237	2 Q6XTC6	Q6xtc6 influenza a
42	1101	93.9	237	2 Q6XTF4	Q6xtf4 influenza a
43	1100	93.9	237	2 Q6XTC8	Q6xtc8 influenza a
44	1100	93.9	237	2 Q6XTE8	Q6xtc8 influenza a
45	1100	93.9	237	2 Q6XTF2	Q6xtf2 influenza a

ALIGNMENTS

RESULT 1
Q6XTI8
ID Q6XTI8 PRELIMINARY; PRT; 237 AA.
AC Q6XTI8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OS Influenza A virus (A/Albany/6/58(H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220953;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210157; AAC46579.1; --
DR HSPB; P03495; IAIL.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 237 AA; 26914 MW; 88C4D124B449BEC3 CRC64;
Query Match 97.5%; Score 1143; DB 2; Length 237;
Best Local Similarity 96.5%; Pred. No. 1.2e-88;
Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDPNTVSSFQVDCFLHVRKQVADQELGDAPFLDLRRDQKSLRGSGTLGLNIETATRA 60
DB 1 MDPNTVSSFQVDCFLHVRKQVADQELGDAPFLDLRRDQKSLRGSGTLGLNIETATRV 60
QY 61 GKQIVERTLKESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQKVAGPLCIRMD 120
DB 61 GKQIVERTLKESDEALKMTWASAPASRYLTDMTTEEMSRDWFMLMPKQKVAGPLCIRMD 120
QY 121 QAIMDKSVILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
DB 121 QAIMDKSVILKANFSVIFDRLETLILRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
QY 181 LIGGLENNNTVRVSKTLQRFAPWSSNENGRPPPTPKQKRWARTIRSEV 230
DB 181 LIGGLENNNTVRVSKTLQRFAPWSSNENGRPPPTPKQKRWARTIRSKV 230
RESULT 2
VNS1_IATUSS
ID VNS1_IATUSS STANDARD; PRT; 237 AA.
AC P03498;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS1.

GN Name=NS; Synonyms=8;
 OS Influenza A virus (strain A/USSR/90/77 H1N1).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A.
 OX NCBI_TaxID=225083;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83164298; PubMed=6834468;
 RA Krystal M., Buonagurio D.A., Young J.P., Palese P.;
 RT "Sequential mutations in the NS genes of influenza virus field
 strains.",
 RL J. Virol. 45:547-554 (1983).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=NS1;
 CC IsoId=P03498-1; Sequence=Displayed;
 CC Name=NS2;
 CC IsoId=P03504-1; Sequence=External;
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; K00578; AAA43540.1; -;
 DR HSSP; P03495; NS1.
 DR InterPro; IPR000256; Flu NS1.
 DR Pfam; PF00600; Flu NS1; 1.
 DR ProDom; PD000613; Flu NS1; 1.
 KW Alternative splicing; Nonstructural protein.
 SQ SEQUENCE 237 AA; 26890 MW; D5759EBE558E268 CRC64;

Query Match 97.4%; Score 1142; DB 1; Length 237;
 Best Local Similarity 97.0%; Pred. No. 1.4e-88;
 Matches 223; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRV 60
 DB 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATCV 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230

RESULT 3
 Q6XTI4 PRELIMINARY; PRT; 237 AA.
 AC Q6XTI4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Non-structural protein NS1.
 OS Influenza A virus (A/Sao Paulo/3/59 (H2N2)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H2N2 subtype.
 OX NCBI_TaxID=220955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lindstrom S.E., Cox N.J., Klimov A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY210159; AA046583.1; -;
 DR HSSP; P03495; IAIL.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR000256; Flu NS1.
 DR InterPro; IPR009068; S15/NS1_bind.
 DR Pfam; PF00600; Flu NS1; 1.
 DR ProDom; PD000613; Flu NS1; 1.
 SQ SEQUENCE 237 AA; 26972 MW; FE0004CAA50CEED7 CRC64;
 Query Match 97.4%; Score 1142; DB 2; Length 237;
 Best Local Similarity 96.5%; Pred. No. 1.4e-88;
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRV 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSKV 230

RESULT 4
 Q6XTI6 PRELIMINARY; PRT; 237 AA.
 AC Q6XTI6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Non-structural protein NS1.
 OS Influenza A virus (A/Victoria/15681/59 (H2N2)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H2N2 subtype.
 OX NCBI_TaxID=220956;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lindstrom S.E., Cox N.J., Klimov A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY210158; AA046581.1; -;
 DR HSSP; P03495; IAIL.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR000256; Flu NS1.
 DR InterPro; IPR009068; S15/NS1_bind.
 DR Pfam; PF00600; Flu NS1; 1.
 DR ProDom; PD000613; Flu NS1; 1.
 SQ SEQUENCE 237 AA; 26972 MW; FE0004CAA50CEED7 CRC64;

Query Match 97.4%; Score 1142; DB 2; Length 237;
 Best Local Similarity 96.5%; Pred. No. 1.4e-88;
 Matches 222; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRA 60
 DB 1 MDPNTVSSFQVDCFLMVRKRVADQELGDAPFLDLRLDQKSLRGSGTLGNIETATRV 60
 QY 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDWMFMPKQKVGAPLCIRMD 120
 QY 121 QAIMDKSIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 DB 121 QAIMDKNIILKANFSVIFDLRLTLILLRAFTTEGAIVGEISPLPSLPGHTNEDIKNAIGV 180
 QY 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSEV 230
 DB 181 LIGGLEWNNNTVRVSKTLQRFAPWSSNENGRPPLTPKQKRWARTIRSKV 230

Best Local Similarity 96.5%; Pred. No. 1.7e-88;
Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRV 60

QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120

QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180

QY 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
DB 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSKV 230

RESULT 8
VNS1_IAPOW STANDARD; PRT; 237 AA.

AC P03497;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS1.
GN Name=8;
OS Influenza A virus (strain A/Fort Warren/1/50 H1N1), and
OS Influenza A virus (strain A/RI/5-/57 H2N2).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OC NCBI_TaxID=225082, 135329;
OX [1]
RN J. Virol. 45:547-554(1983).
RP SEQUENCE FROM N.A.
RC STRAIN=A/Fort Warren/1/50;
RA MEDLINE=83164298; PubMed=6834468;
RX Krystal M., Buonagurio D.A., Young J.F., Palese P.;
RT "Sequential mutations in the NS genes of influenza virus field strains.";
RT J. Virol. 38:1-7(1981).
RL J. Virol. 45:547-554(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A/RI/5-/57;
RX MEDLINE=81218398; PubMed=7241645;
RA Hall R.W., Air G.M.;
RT "Variation in nucleotide sequences coding for the N-terminal regions of the matrix and nonstructural proteins of influenza A viruses.";
RT J. Virol. 38:1-7(1981).
RL J. Virol. 38:1-7(1981).
RN [1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS1;
CC IsoId=P03497-1; Sequence=Displayed;
CC Name=NS2;
CC IsoId=P03505-1; Sequence=External;
CC -1- MISCELLANEOUS: Partial sequence of A/RI/5-/57 is identical with that shown.

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DB EMBL; K00576; AAA43525.1; -.
DR HSSP; P03495; lNS1.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.

KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 237 AA; 26889 MW; 3B80159BFD79F212 CRC64;

Query Match 97.3%; Score 1140; DB 1; Length 237;
Best Local Similarity 96.5%; Pred. No. 2.1e-88;
Matches 222; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRV 60

QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120

QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180

QY 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
DB 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230

RESULT 9
Q6XTJ4 PRELIMINARY; PRT; 237 AA.

AC Q6XTJ4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OS Influenza A virus (A/Chile/13/57(H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype-1
OX NCBI_TaxID=221934;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210154; AAC46573.1; -.
DR HSSP; P03495; lAIL.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 237 AA; 27004 MW; 29158F214298F365 CRC64;

Query Match 97.2%; Score 1139; DB 2; Length 237;
Best Local Similarity 96.1%; Pred. No. 2.5e-88;
Matches 221; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRA 60
DB 1 MDPNTVSSFOVDCFLWHVRKRVADQELGDAPFLDLRLRDQKSLRGSTGLGNIETAIRV 60

QY 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTWASAPASRYLTDMTIEEMSRDWMFLMPKQKVAGPLCIRMD 120

QY 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTGAIVGEISPLSPGHTNEDIKNAIGV 180

QY 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSEV 230
DB 181 LIGGLEWNNNTVRSKTLQRFARWSSNENGRPPLTPKQKRMARTIRSKV 230

RESULT 10
Q6XTJ8 PRELIMINARY; PRT; 237 AA.

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AC Q6XTJ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OC Influenza A virus (A/Albany/7/57 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=135321;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210152; AAO46569.1; -.
DR HSSP; P03495; IAIL.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
DR SEQUENCE 237 AA; 26944 MW; AA82935CF4533C5C CRC64;

Query Match          97.1%; Score 1138; DB 2; Length 237;
Best Local Similarity 96.1%; Pred. No. 3.1e-88;
Matches 221; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDPNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATRV 60
Db 1 MDPNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATRV 60
Qy 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
Db 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLSPFGHTNEDIKNAIGV 180
Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLSPFGHTNEDIKNAIGV 180
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSKV 230

RESULT 11
Q6XTI2 PRELIMINARY; PRT; 230 AA.
AC Q6XTI2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OC Influenza A virus (A/Philippines/2/60 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=221935;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210160; AAO46585.1; -.
DR HSSP; P03495; IAIL.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
DR SEQUENCE 230 AA; 26089 MW; 0A6DE9DEF3019F70 CRC64;

Query Match          96.3%; Score 1129; DB 2; Length 230;
Best Local Similarity 95.7%; Pred. No. 1.7e-87;
Matches 220; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDPNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATRA 60

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Db 1 MDSNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATRV 60
Qy 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
Db 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLSPFGHTNEDIKNAIGV 180
Db 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLSPFGHTNEDIKNAIGV 180
Qy 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFARWSSNENGRPPLTPKQKRWARTIRSKV 230

RESULT 12
VNS1_IACHI
ID_VNS1_IACHI STANDARD; PRT; 237 AA.
AC P11618;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nonstructural protein NS1.
GN Name=8;
OS Influenza A virus (strain A/Chile/1/83 H1N1).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=241242;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345097; PubMed=2762132;
RT Schreier E., Roeseke H., Michel S.;
RT "Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83
   (H1N1).";
RL Nucleic Acids Res. 17:5381-5381 (1989).
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS1;
CC IsoId=P11618-1; Sequence=Displayed;
CC Name=NS2;
CC IsoId=P11619-1; Sequence=External;
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15282; CAA33355.2; -.
CC HSSP; P03495; INS1.
CC InterPro; IPR000256; Flu NS1.
CC InterPro; IPR009068; S15/NS1_bind.
CC Pfam; PF00600; Flu NS1; 1.
CC ProDom; PD000613; Flu NS1; 1.
CC Alternative splicing; Nonstructural protein.
SQ SEQUENCE 237 AA; 26819 MW; C33A9E3D0386E752 CRC64;

Query Match          96.2%; Score 1128; DB 1; Length 237;
Best Local Similarity 95.2%; Pred. No. 2.2e-87;
Matches 219; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDPNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATRA 60
Db 1 MDPNTVSSQVDCFLHWVRKVADQELGDAPEFLDLRRDQKSLRGSGTLGLNIETATCV 60
Qy 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCIRMD 120
Db 61 GQOIVERILKEESDEALKMTWASAPASRYLTDMTTEEMSRDWMFMPKQKVAGPLCVRMD 120
Qy 121 QAIMDKSIILKANFSVIFDRLETLILLRAFTBEGAIVGEISPLSPFGHTNEDIKNAIGV 180

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Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230

RESULT 13
Q6XTJ0 PRELIMINARY; PRT; 237 AA.
AC Q6XTJ0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Non-structural protein NS1.
OS Influenza A virus (A/Malaya/16/58(H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220954;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY210156; AA046577.1; -.
DR HSSP; P03495; 1A1L.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 237 AA; 26940 MW; 60BBC406AFD784C9 CRC64;

Query Match 96.0%; Score 1125; DB 2; Length 237;
Best Local Similarity 95.2%; Pred. No. 3.9e-87; Mismatches 5; Indels 0; Gaps 0;
Matches 219; Conservative 6;

QY 1 MDPNTVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETAIRA 60
Db 1 MDPNTVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRV 60
QY 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDFWMLMPKQKVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDFWMLMPKQKVAGPLCIRMD 120
QY 121 QAIMDKSIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230

RESULT 14
Q82505 PRELIMINARY; PRT; 230 AA.
AC Q82505;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Non-structural protein 1.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A/WSN/40; TISSUE=Mouse;
RA Husak P.J., Schlesinger R.W.;
RT "Replication of neurovirulent and non-neurovirulent human H1N1
influenza A viruses in mouse brain and nerve cell cultures: virus

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strain-specific and host cell-dependent variations in progeny virus
asse.";
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert
Wood Johnson Medical School.
DR EMBL; U13682; AAA21580.1; -.
DR HSSP; P03495; 1NS1.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26040 MW; 03D355F2EA3AC5A8 CRC64;

Query Match 95.9%; Score 1124; DB 2; Length 230;
Best Local Similarity 94.8%; Pred. No. 4.6e-87;
Matches 218; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPNTVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETAIRA 60
Db 1 MDPNTVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLDIETATRA 60
QY 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDFWMLMPKQKVAGPLCIRMD 120
Db 61 GKQIVERILKEESDEALKMTMASAPASRYLTDMTIEEMSRDFWMLMPKQKVAGPLCIRMD 120
QY 121 QAIMDKSIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVSIFDRLETLILLRAFTBEGAIVGEISPLSPGHTDVEDVKNAGV 180
QY 181 LIGGLEWNNNTVRVSKTLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230
Db 181 LIGGLEWNNNTVRVSETLQRFWRSSNENGRPLTPKQKRWARTIRSEV 230

RESULT 15
Q84068 PRELIMINARY; PRT; 233 AA.
AC Q84068;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Nonstructural protein 1 (Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86208139; PubMed=2939560;
RA Buonagurio D.A., Nakada S., Parvin J.D., Krystal M., Palese P.,
RA Fitch W.M.;
RT "Evolution of human influenza A viruses over 50 years: rapid, uniform
rate of change in NS gene.";
RL Science 232:980-982(1986).
DR EMBL; M12592; AAA43506.1; -.
DR HSSP; P03495; 1NS1.
DR GO; GO:0019012; C:virion; IEA.
DR InterPro; IPR000256; Flu NS1.
DR InterPro; IPR009068; S15/NS1_bind.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
KW Nonstructural protein.
PT NON TER 1
SQ SEQUENCE 233 AA; 26485 MW; 1C345B24E04D617D CRC64;

Query Match 95.8%; Score 1123; DB 2; Length 233;
Best Local Similarity 96.9%; Pred. No. 5.6e-87;
Matches 219; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETAIRAQKI 64
Db 1 TVSSFQVDCFLMHVVRKRVADQELGDPFLDRLRDQKSLRGSGTLGLNIETATRVGKI 60

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Qy	65	VERILKEESDEALKQMTMASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMDQAIM	124
Db	61	VERILKEESDEALKQMTMASAPASRYLTDMTTEMSRDWFMMPKQKVAGPLCIRMDQAIM	120
Qy	125	DKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPGLPHTNEDIKNAIGVLIGG	184
Db	121	DKSIILKANFSVIFDRLETLILLRAFTTEGAIVGEISPLPGLPHTNEDIKNAIGVLIGG	180
Qy	185	LEWNNNTVRVSKTLQRFARSSNENGRPPLTPKQKRWARTIRSEV	230
Db	181	LEWNNNTVRVSKTLQRFARSSNENGRPPLTPKQKRWARTIRSEV	226

Search completed: September 22, 2005, 21:46:05
Job time : 145.504 secs

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:28:42 ; Search time 82.3903 Seconds
(without alignments)
568.004 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFQILMRISKWQ.....ALQLLVEQRIRTFQFLI 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseq1980s.*

2: geneseq1990s.*

3: geneseq2000s.*

4: geneseq2001s.*

5: geneseq2002s.*

6: geneseq2003as.*

7: geneseq2003bs.*

8: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	97.2	121	5 AAE23117	Aae23117 Influenza
2	575	94.7	121	5 ABB05773	Abb05773 Influenza
3	96.5	15.9	880	4 AAB96332	Aab96332 Putative
4	96.5	15.9	880	8 ADS43213	Ads43213 Bacterial
5	86	14.2	819	4 RAM40442	Ram40442 Human pol
6	86	14.2	819	4 RAM40443	Ram40443 Human pol
7	86	14.2	819	8 ADS11970	Ads11970 Human the
8	86	14.2	819	8 ADS11971	Ads11971 Human the
9	86	14.2	819	8 ADS11969	Ads11969 Human the
10	86	14.2	819	8 ADS11968	Ads11968 Human the
11	84	13.8	122	5 AAE23128	Aae23128 Influenza
12	83.5	13.8	1179	8 ADS41964	Ads41964 Bacterial
13	83.5	13.8	1179	8 ADN18677	Adn18677 Bacterial
14	83	13.7	996	4 ABB71614	Abb71614 Drosophil
15	82.5	13.6	236	7 ADN95580	Adn95580 Human BEC
16	82	13.5	350	2 AAY37571	Aay37571 Chlamydia
17	82	13.5	561	2 RAM63043	Ram63043 Streptoco
18	82	13.5	876	7 ADM26084	Adm26084 Hyperther
19	81	13.3	156	2 AAR03991	Aar03991 Mr 25K in
20	81	13.3	498	7 ADF74149	Adf74149 Human nov
21	81	13.3	653	8 ADO66256	Ado66256 Novel hum
22	81	13.3	872	5 AAO22902	Aao22902 Phosphati
23	81	13.3	872	5 ABU65076	Abu65076 Human NOV
24	81	13.3	872	8 ADN61803	Adn61803 Human nov
25	81	13.3	874	5 ABP69419	Abp69419 Human pol

26	81	13.3	874	5 ABG31896	Abg31896 Human lip
27	81	13.3	874	5 AAU79749	Aau79749 Human pho
28	81	13.3	881	8 ADQ66093	Adq66093 Novel hum
29	81	13.3	902	5 ABG31895	Abg31895 Human lip
30	81	13.3	902	5 AAU79750	Aau79750 Human pho
31	80.5	13.3	163	4 ABG06887	Abg06887 Novel hum
32	80.5	13.3	944	6 ABR53314	AbR53314 Protein s
33	80.5	13.3	944	7 ADK63498	Adk63498 Disease t
34	80.5	13.3	944	8 ADN19029	Adn19029 Bacterial
35	80	13.2	376	8 ADN22707	Adn22707 Bacterial
36	80	13.2	875	5 AAO22903	Aao22903 Phosphati
37	80	13.2	952	7 ADJ69356	Adj69356 Human hea
38	80	13.2	962	3 AAB13326	Aab13326 Caenorhab
39	80	13.2	1131	8 ABM80698	Abm80698 Tumour-as
40	80	13.2	1253	4 AAB47149	Aab47149 CDIFF-8,
41	80	13.2	1281	8 ADP55147	Adp55147 Human PRO
42	80	13.2	1281	8 ADP24771	Adp24771 PRO polyp
43	77.5	12.8	331	7 ADF06826	Adf06826 Bacterial
44	77.5	12.8	777	8 ADQ66447	Adq66447 Novel hum
45	77.5	12.8	2000	8 ADN03898	Adn03898 Antipsori

ALIGNMENTS

RESULT 1
AAE23117
ID AAE23117 standard; protein; 121 AA.
XX
AC AAE23117;
XX
AC AAE23117;
DT 21-AUG-2002 (first entry)
DE Influenza A virus/singapore/1/57/ca NS2 mutant protein.
XX
DE Attenuated influenza vaccine; prophylactic; therapeutic; infection;
KW virucide; mutant; mutein; NS2 protein.
XX
OS Influenza A virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 8..9 /note= "Encoded by 48-525 bases"
XX
XX WO200224876-A2.
PD 28-MAR-2002.
XX
XX 25-SEP-2001; 2001WO-EP011087.
XX
XX 25-SEP-2000; 2000EP-00120896.
XX
XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX
XX Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;
XX
XX WPI: 2002-416282/44.
XX
XX N-PSDB; AAD37061.
XX
XX Manufacturing live vaccine, by infecting Vero cells with virus, combining
XX cells with serum-free cell culture medium, incubating cells in presence
XX of protease and nuclease, harvesting virus and preparing vaccine.
XX
XX Example 4; Page 63; 90pp; English.
XX
XX The present invention relates to a method for isolating viruses from
XX various sources and for producing live attenuated influenza vaccines in a
XX serum-free African Green monkey kidney (Vero) cell culture under
XX conditions where alterations in the surface antigens of the virus due to
XX adaptive selection are minimised or prevented. The method is useful for
XX the manufacture of whole-virus vaccine, preferably attenuated live
XX vaccine. It is useful for prophylactic or therapeutic administration

CC represent Influenza A/Quinn/72 (H3N2) strain sequencing primers) which
CC are used in an example from the present invention

20 OLG-SSSEDLNGIITOFESLKYRDSLGEAVMRMGDLHSLQNRNGKWREQLGQKFE--E 75

[illegible]

CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 819 AA;
 SQ
 Query Match 14.2%; Score 86; DB 4; Length 819;
 Best Local Similarity 21.5%; Pred. No. 2.1;
 Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;
 Qy 19 MQLGSSSEDLNGIITQFESLKLRYDSLGEAVM-RMGDLHSLQNRNGKWRQQLGQ----- 71
 Db 537 LPIGTASADVAADIADK-----YTSKLMDAIKGTMTIYNDLSKNTTWKAQLAEDSQGLR 590
 Qy 72 -KFEIRWL-----IEEVHRLKITEENSFEQITFMQALQLLLEVEOEI 113
 Db 591 IEIEKQLWLHQQLSEMKHNLTLTMAEMRQSWEQERDLIAEVKKQL 637
 RESULT 6
 AAM40443
 ID AAM40443 standard; protein; 819 AA.
 XX AC AAM40443;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 5374.
 XX KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX OS Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US034263.
 XX PR 23-DEC-1999; 99US-00471275.
 XX PR 21-JAN-2000; 2000US-00498725.
 XX PR 25-APR-2000; 2000US-00552317.
 XX PR 20-JUN-2000; 2000US-00598042.
 XX PR 19-JUL-2000; 2000US-00620312.
 XX PR 03-AUG-2000; 2000US-00653450.
 XX PR 14-SEP-2000; 2000US-00662191.
 XX PR 19-OCT-2000; 2000US-00693036.
 XX PR 29-NOV-2000; 2000US-00727344.
 XX PA (HYSEQ-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 XX N-PSDB; AAI59599.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 XX as central nervous system injuries.
 XX Example 2; SEQ ID NO 5374; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 819 AA;
 SQ
 Query Match 14.2%; Score 86; DB 4; Length 819;
 Best Local Similarity 21.5%; Pred. No. 2.1;
 Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;
 Qy 19 MQLGSSSEDLNGIITQFESLKLRYDSLGEAVM-RMGDLHSLQNRNGKWRQQLGQ----- 71
 Db 537 LPIGTASADVAADIADK-----YTSKLMDAIKGTMTIYNDLSKNTTWKAQLAEDSQGLR 590
 Qy 72 -KFEIRWL-----IEEVHRLKITEENSFEQITFMQALQLLLEVEOEI 113
 Db 591 IEIEKQLWLHQQLSEMKHNLTLTMAEMRQSWEQERDLIAEVKKQL 637
 RESULT 7
 ADS11970
 ID ADS11970 standard; protein; 819 AA.
 XX AC ADS11970;
 XX DT 16-DEC-2004 (first entry)
 XX DE Human therapeutic contig protein - SEQ ID 2207.
 XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .819
 FT /label= Unknown, OTHER
 FT /note= "OTHER = In-frame STOP codon"
 XX WO2004080148-A2.
 XX 23-SEP-2004.
 XX 30-SEP-2003; 2003WO-US030720.
 XX 02-OCT-2002; 2002US-0416186P.
 XX (NUVE-) NUVELO INC.
 XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 XX WPI; 2004-668857/65.
 XX N-ESDB; ADS11372.
 XX New polynucleotide, useful in preparing a composition for diagnosing or
 XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 XX aplastic anemia or cancer for promoting wound healing.

PS Example 2; SEQ ID NO 2207; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC protein of the invention.

XX Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1;

Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

QY 19 MQLGSSSEDLNGIITQESLKYRDSIGEAVM-RMGDLHSLQNGKWRQELGQ----- 71

DB 537 LPIGTASADVAADIATK-----YTSKLMDAIGKMTIYNDLSKNTTWKQAELDSQGLR 590

QY 72 -KPEEIRWL-----IEVVRHLKITENSFEQITFMQALQLLLEVRQEI 113

DB 591 IEIEKQLWLHQQLSEKKNLELTMAEMRQSWEQERDLIAEVKKQL 637

RESULT 8

ADSL1971

ID ADSL1971 standard; protein; 819 AA.

XX AC ADSL1971;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig protein - SEQ ID 2208.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;

XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

XX aplastic anaemia; cancer; wound healing; gene therapy.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 1. .819

XX /label= Unknown, OTHER

XX /note= "OTHER = In-frame STOP codon"

XX W02004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;

XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

XX N-PSDB; ADS11373.

XX New polynucleotide, useful in preparing a composition for diagnosing or

XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,

XX aplastic anaemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2208; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded

XX polypeptide. The molecules of the invention demonstrate antiinflammatory,

XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may

XX be useful in preparing a composition for diagnosing or treating

XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell

XX disorders, such as aplastic anaemia or cancer, as well as for promoting

XX wound healing. The molecules may also be utilised during gene therapy

XX procedures. The current sequence is that of a human therapeutic contig

XX protein of the invention.

XX Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1;

Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

QY 19 MQLGSSSEDLNGIITQESLKYRDSIGEAVM-RMGDLHSLQNGKWRQELGQ----- 71

DB 537 LPIGTASADVAADIATK-----YTSKLMDAIGKMTIYNDLSKNTTWKQAELDSQGLR 590

QY 72 -KPEEIRWL-----IEVVRHLKITENSFEQITFMQALQLLLEVRQEI 113

DB 591 IEIEKQLWLHQQLSEKKNLELTMAEMRQSWEQERDLIAEVKKQL 637

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CC protein of the invention.

XX Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1; Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

QY 19 MQLGSSSEDLNGIITQFESLKYRDSLGEAVM-RMGDLHSLQNRNGKWRQOLGQ-----71

DB 537 LPIGTASADVADIADK-----YTSKLMADKGTMTIYNDLSKNTTWKQALAEQSGLR 590

QY 72 -KFEIRWL-----IEVVRHLKITENSFEQITFMQALQLLLEVEQEI 113

DB 591 IEIEKQLWLHQELSEMKNHLELTMAEMRQSEWQERDLIAEVKKQL 637

RESULT 10

ADSL1968

ID ADSL1968 standard; protein; 819 AA.

AC ADSL1968;

XX 16-DEC-2004 (first entry)

DE Human therapeutic contig protein - SEQ ID 2205.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;

KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;

KW aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..819

FT /label= Unknown, OTHER

FT /note= "OTHER = In-frame STOP codon"

PN WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;

PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX WPI; 2004-668857/65.

DR N-PSDB; ADSL1370.

XX New polynucleotide, useful in preparing a composition for diagnosing or

PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,

PT aplastic anemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2205; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded

CC polypeptide. The molecules of the invention demonstrate antiinflammatory,

CC neuroprotective, antianaemic, cytostatic and vulnery activities and may

CC be useful in preparing a composition for diagnosing or treating

CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell

CC disorders, such as aplastic anaemia or cancer, as well as for promoting

CC wound healing. The molecules may also be utilised during gene therapy

CC procedures. The current sequence is that of a human therapeutic contig

CC protein of the invention.

XX Sequence 819 AA;

Query Match 14.2%; Score 86; DB 8; Length 819;

Best Local Similarity 21.5%; Pred. No. 2.1;

Matches 23; Conservative 32; Mismatches 34; Indels 18; Gaps 4;

QY 19 MQLGSSSEDLNGIITQFESLKYRDSLGEAVM-RMGDLHSLQNRNGKWRQOLGQ-----71

DB 537 LPIGTASADVADIADK-----YTSKLMADKGTMTIYNDLSKNTTWKQALAEQSGLR 590

QY 72 -KFEIRWL-----IEVVRHLKITENSFEQITFMQALQLLLEVEQEI 113

DB 591 IEIEKQLWLHQELSEMKNHLELTMAEMRQSEWQERDLIAEVKKQL 637

RESULT 11

AAE23128

ID AAE23128 standard; protein; 122 AA.

XX AAE23128;

XX 21-AUG-2002 (first entry)

DE Influenza B virus/vienna/1/99/ca NS2 mutant protein.

KW Attenuated influenza vaccine; prophylactic; therapeutic; infection;

KW virucide; mutant; mutein; NS2 protein.

OS Influenza B virus.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "Wild type Tle substituted with Thr"

FT Misc-difference 7 /note= "Wild type Tle substituted with Thr"

FT Misc-difference 11..12 /note= "Encoded by 74-734 bases"

FT /note= "Encoded by 74-734 bases"

PN WO200224876-A2.

XX 28-MAR-2002.

XX 25-SEP-2001; 2001WO-EF011087.

XX 25-SEP-2000; 2000EP-00120896.

XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX Katinger H, Egorov A, Ferko B, Romanova J, Katinger D;

XX WPI; 2002-416282/44.

DR N-PSDB; AAD37069.

XX Manufacturing live vaccine, by infecting Vero cells with virus, combining

PT cells with serum-free cell culture medium, incubating cells in presence

PT of protease and nuclease, harvesting virus and preparing vaccine.

XX Example 4; Page 90; 90pp; English.

XX The present invention relates to a method for isolating viruses from

CC various sources and for producing live attenuated influenza vaccines in a

CC serum-free African Green monkey kidney (Vero) cell culture under

CC conditions where alterations in the surface antigens of the virus due to

CC adaptive selection are minimised or prevented. The method is useful for

CC the manufacture of whole-virus vaccine, preferably attenuated live

CC vaccine. It is useful for prophylactic or therapeutic administration

CC against viral infection, preferably influenza virus infections. The

CC present sequence is influenza B virus/vienna/1/99/ca (cold adapted) NS2

CC mutant protein. This sequence is used in the exemplification of the

CC invention

XX Sequence 122 AA;

Query Match 13.8%; Score 84; DB 5; Length 122;

Best Local Similarity 25.0%; Pred. No. 0.26;

Matches 34; Conservative 24; Mismatches 44; Indels 34; Gaps 6;

QY 4 NTVSFDDILMRISKMGSSSED-----LNGIITQFESLKYRDSLGEAVMRMGDLHSLQ 59
 Db 3 NNITTTQ-IEWRMKKAIGSTHSSSSVLMKDIOQFQKLKRWESYPLV-KSTDYH--- 57
 QY 60 NRMGKWEQLGQKFEIRWLIEVR-----HRLKITENSF--EQITFMQALQL 105
 Db 58 -----QKRETKLVTEELYLLSKRIDNLLFKHTVIANSSIIADNVVLSLLET 106
 QY 106 LLEVEQBIRTFSQLI 121
 Db 107 LYEMKDVVEYSROCL 122

RESULT 12
 ADS41964
 ID ADS41964 standard; protein; 1179 AA.
 XX ADS41964;
 XX
 DT 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #20394.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS
 XX US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 20394; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1179 AA;

Query Match 13.8%; Score 83.5; DB 8; Length 1179;
 Best Local Similarity 23.9%; Pred. No. 6.6;
 Matches 27; Conservative 27; Mismatches 44; Indels 15; Gaps 3;

QY 23 SSSDNLNGIITQF-----ESLKYRDSLGEAVMRMGDLHSLQNRNGKWEQLGQ 71
 Db 825 SLEEEIEGLVKNKALKANINENEALKSLTEKLEKKEGEIYSRIEEQKKKEBLER 894
 QY 72 KFEIRWLIEVRH---LKITENSFEQITFMQALQLLLEVEQBIRTFSQLI 121
 Db 885 KVAELREEKEKISRRIQELRIEVNLT-KVRNSQLKSLMEKNSQLKHSKEVI 936

RESULT 13
 ADN18677
 ID ADN18677 standard; protein; 1179 AA.
 XX ADN18677;
 XX
 DT 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #1330.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS
 XX US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 1330; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a

microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Query Match 13.8%; Score 83.5; DB 8; Length 1179;
Best Local Similarity 23.9%; Pred. No. 6.6;
Matches 27; Conservative 27; Mismatches 44; Indels 15; Gaps 3;

QY 23 SSEDNGIITQP-----ESLKLYRDSIGEAVMRGMGLHSLQNRNGKWRQLGQ 71
DB 825 SLEEEGLVKNKALKANINNEEAUKSITKLEKUKKEEGYRIEIEQKKKCELER 884
QY 72 KPEIRWLEIEVRHR---LKITENSFEQITFMQALQLLLEVEQIRTFSPQLI 121
DB 885 KVAREEKEKISRRIQELRIEVTNL-KVNSQLKSLMEKNSQLKHFSKEVI 936

RESULT 14
ABB71614
ID ABB71614 standard; protein; 996 AA.
AC ABB71614;
XX
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 41634.
XX Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX Drosophila melanogaster.
XX W0200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL15717.
XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
XX Disclosure; SEQ ID NO 41634; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLL16176-ABL30511), expressed DNA sequences (ABLL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fcp.wipo.int/pub/published_pct_sequences

XX Sequence 996 AA;

Query Match 13.7%; Score 83; DB 4; Length 996;
Best Local Similarity 26.1%; Pred. No. 6;
Matches 31; Conservative 25; Mismatches 39; Indels 24; Gaps 5;

QY 2 DNTVSSFDILMRISKMQLGSSSEDLNGLIITQFESLKLYRDSIGEAVMRGMGLH----- 56
DB 824 DPEQI---QQLQSGVGLQ---SGEGLEG-----ETLQMTDGGQMLVHGDNNBOQLI 872
QY 57 --SLQNRNGKWRQLGQKPEIRWLEIEVRHRKLTENSFEQITFMQALQLLLEVEQEI 113
DB 873 DASLLNSEQLLIQQQDGEAGNVISEDGTIRIPVS-----VSYTEDGQPIVQVQQV 925

RESULT 15
ADN95580
ID ADN95580 standard; protein; 236 AA.
XX ADN95580;
XX 01-JUL-2004 (first entry)
XX Human BEC/LEC-related protein sequence SeqID503.

XX growth; differentiation; blood endothelial cell; BEC;
XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
XX lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
XX vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
XX inflammatory disease; cancer metastasis; lymphatic system; human.

OS Homo sapiens.
XX W02003080640-A1.
XX 02-OCT-2003.
XX 07-MAR-2003; 2003WO-US006900.
XX 07-MAR-2002; 2002US-0363019P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
XX N-PSDB; ADN95581.

XX Example 1; SEQ ID NO 503; 176pp; English.

XX This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:33:28 ; Search time 16.8917 Seconds
(without alignments)
689.226 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFDILMRISKMQ.....ALQLLVEQEIRTFSQLI 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	98.4	121	1 MNIV2A	nonstructural prot
2	596	98.2	121	2 S33685	nonstructural prot
3	594	97.9	121	1 MNIV62	nonstructural prot
4	588	96.9	121	1 MNIV2M	nonstructural prot
5	587	96.7	121	1 MNIVC2	nonstructural prot
6	586	96.5	121	1 MNIV2W	nonstructural prot
7	575	94.7	121	1 B45539	nonstructural prot
8	575	94.7	121	1 MNIV2K	nonstructural prot
9	574	94.6	121	2 S09649	NS2 protein - infl
10	569	93.7	118	1 MNIVXX	nonstructural prot
11	567	93.4	121	1 MNIV2	nonstructural prot
12	564	92.9	118	1 MNIVX4	nonstructural prot
13	564	92.9	118	1 MNIVX8	nonstructural prot
14	564	92.9	121	1 MNIVB4	nonstructural prot
15	563	92.8	121	1 MNIVB1	nonstructural prot
16	559	92.1	121	1 MNIVB3	nonstructural prot
17	556	91.6	118	1 MNIVX2	nonstructural prot
18	549	90.4	118	1 MNIVX6	nonstructural prot
19	517	85.2	108	1 MNIV2F	nonstructural prot
20	486	80.1	121	1 MNIV26	nonstructural prot
21	478	78.7	121	2 B45575	nonstructural prot
22	475	78.3	121	1 MNIVB7	nonstructural prot
23	473	77.9	121	1 MNIVB5	nonstructural prot
24	468	77.1	121	1 MNIVB6	nonstructural prot
25	467	76.9	121	1 MNIVB8	nonstructural prot
26	96.5	15.9	880	2 F75103	conserved hypothet
27	88	14.5	2541	2 T29340	hypothetical prote
28	83.5	13.8	1179	2 F71190	probable chromosom
29	82.5	13.6	122	1 MNIVB	nonstructural prot

ALIGNMENTS

RESULT 1

MNIV2A

nonstructural protein NS2 - influenza A virus (strain A/USSR/90/77 [H1N1])

C;Species: influenza A virus

C;Date: 31-Oct-1980 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999

C;Accession: B92991; A04095; A90801; C92991; D92991

R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: B92991

A;Molecule type: genomic RNA

A;Residues: 1-121 <RRY>

A;Cross-references: GB:K00578; NID:g324839; PIDN:AAA43539.1; PID:g324840

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 98.4%; Score 597; DB 1; Length 121;
Best Local Similarity 97.5%; Pred. No. 2.6e-44;
Matches 118; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	1	MDPNTVSSFDILMRISKMQLGSSSEDLMGITQPFESLKYRDSLGAVNRMGDLHSLQN	60
DB	1	MDPNTVSSFDILMRISKMQLGSSSEDLMGITQPFESLKYRDSLGAVNRMGDLHSLQN	60
QY	61	RNGKWEQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLVEQEIRTFSQL	120
DB	61	RNGKWEQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLVEQEIRTFSQL	120
QY	121	I 121	
DB	121	I 121	

RESULT 2

S33685

nonstructural protein NS1 - influenza A virus (strain A/WS/33)

C;Species: influenza A virus

A;Variety: strain A/WS/33

C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: S33685; S32221

R;Ward, A.C.; Azad, A.A.; Macreadie, I.G.; McKimm-Breschkin, J.L.

Nucleic Acids Res. 21, 2257, 1993

A;Title: Complete nucleotide sequence of the non-structural gene of the human influenza

A;Reference number: S33685; MUID:93275765; PMID:8502573

A;Accession: S33685

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-121 <WAR>

A;Cross-references: UNIPROT:Q06049; EMBL:Z21498; NID:g296585; PIDN:CAA79707.1; PID:g2965.

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C:Genetics:

A:Map position: segment 8

C:Superfamily: influenza virus nonstructural protein NS2

C:Keywords: alternative splicing

Query Match 98.2%; Score 596; DB 2; Length 121;
Best Local Similarity 98.3%; Pred. No. 3.1e-44;
Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 3

MNV62

nonstructural protein NS2 - influenza A virus (strain A/Ann Arbor/6/60 [H2N2])

C:Species: influenza A virus

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999

C:Accession: H31831

R:Cox, N.J.; Kitame, F.; Kendal, A.P.; Maassab, H.F.; Naeve, C.

Virology 167, 554-567, 1988

A:Title: Identification of sequence changes in the cold-adapted, live attenuated influenza

A:Reference number: A31831; MUID:89073759; PMID:2974219

A:Accession: H31831

A:Molecule type: genomic RNA

A:Residues: 1-121 <CX>

A:Cross-references: GB:M23968; GB:J04349; GB:M23969; NID:G324860; PIDN:AAA43552.1; PID:9

C:Genetics:

A:Map position: segment 8

A:Introns: 10/3

C:Superfamily: influenza virus nonstructural protein NS2

C:Keywords: alternative splicing; nonstructural protein

Query Match 97.9%; Score 594; DB 1; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.6e-44;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 4

MNV2M

nonstructural protein NS2 - influenza A virus (strain A/FM/1/47 [H1N1])

C:Species: influenza A virus

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999

C:Accession: D92991; A04095

R:Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A:Title: Sequential mutations in the NS genes of influenza virus field strains.

A:Reference number: A92991; MUID:83164298; PMID:6834468

A:Accession: D92991

A:Molecule type: genomic RNA

A:Residues: 1-121 <KRY>

A:Cross-references: GB:K00576; NID:G324813; PIDN:AAA43524.1; PID:G324814

C:Genetics:

A:Map position: segment 8

C:Superfamily: influenza virus nonstructural protein NS2

C:Keywords: alternative splicing

Query Match 96.9%; Score 588; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.5e-43;
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 5

MNV2C

nonstructural protein NS2 - influenza A virus (strain A/Chile/1/83 [H1N1])

C:Species: influenza A virus

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jul-1999

C:Accession: B34215; S04837

R:Schreier, E.; Roeseke, H.; Michel, S.

Nucleic Acids Res. 17, 5381, 1989

A:Title: Nucleotide sequence of the NS gene of influenza virus A/Chile/1/83 (H1N1).

A:Reference number: A34215; MUID:89345097; PMID:2762132

A:Accession: B34215

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-121 <SCH>

A:Cross-references: EMBL:X15282; NID:G60479; PIDN:CAA33356.1; PID:G60481

C:Genetics:

A:Map position: segment 8

A:Introns: 10/3

C:Superfamily: influenza virus nonstructural protein NS2

C:Keywords: alternative splicing; nonstructural protein

Query Match 96.7%; Score 587; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.8e-43;
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKMGSSSEDNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGWREQLGQKFEIRWLIEVRHRLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 6

MNV2W

nonstructural protein NS2 - influenza A virus (strain A/FW/1/50 [H1N1])

C:Species: influenza A virus

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999

C:Accession: C92991; A04095

R:Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.

J. Virol. 45, 547-554, 1983

A:Title: Sequential mutations in the NS genes of influenza virus field strains.

A:Reference number: A92991; MUID:83164298; PMID:6834468

A:Accession: C92991

A:Molecule type: genomic RNA

A:Residues: 1-121 <KRY>

A;Cross-references: GB:K00577; NID:G324808; PIDN:AAA43521.1; PID:G324809
C;Genetics:
A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS2
C;Keywords: alternative splicing

Query Match 96.5%; Score 586; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 2.2e-43;
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 7

E45539

nonstructural protein NS2 - influenza A virus (strain A/chicken/Brescia/1902 [H7N7])

C;Species: influenza A virus

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 26-May-1994

C;Accession: E45539

R;Klimov, A.; Prosech, S.; Schafer, J.; Bucher, D.

Arch. Virol. 122, 143-161, 1992

A;Title: Subtype H7 influenza viruses: comparative antigenic and molecular analysis of

A;Reference number: A45539; MUID:92109567; PMID:1530908

A;Accession: E45539

A;Molecule type: genomic RNA

A;Residues: 1-121 <KUI>

A;Note: sequence extracted from NCBI backbone (NCBIN:74250, NCBIIP:74255)

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;

Best Local Similarity 94.2%; Pred. No. 2e-42;

Matches 114; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDSNTVSSFDILMRISKQMGSSSEDLNGMITQFETLKLYRDSLGAVMRIGDLHSLQS 60

Qy 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 8

MNIV2K

nonstructural protein NS2 - influenza A virus (strains A/Alaska/6/77 and A/Udorn/72 [H3N

C;Species: influenza A virus

A;Note: host Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004

C;Accession: A04094; A90801; A04095

R;Buonsquiro, D.A.; Krystal, M.; Palese, P.; DeBorde, D.C.; Maassab, H.F.

J. Virol. 49, 418-425, 1984

A;Title: Analysis of an influenza A virus mutant with a deletion in the NS segment.

A;Reference number: A92994; MUID:84115066; PMID:6363726

A;Accession: A04094

A;Molecule type: genomic RNA

A;Residues: 1-121 <BUO>

A;Cross-references: UNIPROT:P03503; GB:K01332; NID:G324795; PIDN:AAA43514.1; PID:G324796
A;Experimental source: strain A/Alaska/6/77
R;Lamb, R.A.; Lai, C.J.

Cell 21, 475-485, 1980

A;Title: Sequence of interrupted and uninterrupting mRNAs and cloned DNA coding for the v

A;Reference number: A90801; MUID:81001890; PMID:7407920

A;Accession: A90801

A;Molecule type: genomic RNA

A;Residues: 1-121 <LAM>

A;Cross-references: GB:V01102; GB:J02169; NID:G60797; PIDN:CAA24289.1; PID:G60799

A;Experimental source: strain A/Udorn/72 [H3N2]

C;Genetics:

A;Map position: segment 8

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

C;Keywords: alternative splicing

Query Match 94.7%; Score 575; DB 1; Length 121;

Best Local Similarity 94.2%; Pred. No. 2e-42;

Matches 114; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDSNTVSSFDILMRISKQMGSSSEDLNGMITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 9

S09649

NS2 protein - influenza A virus

C;Species: influenza A virus

C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jul-2000

C;Accession: S09649

R;Baklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mama

Bioorg. Khim. 11, 641-645, 1985

A;Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 o

A;Reference number: S09648; MUID:85307107; PMID:4038350

A;Accession: S09649

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-121 <BEK>

A;Cross-references: EMBL:X52146; NID:G60716; PIDN:CAB38574.1; PID:G4490559

C;Genetics:

A;Introns: 10/3

C;Superfamily: influenza virus nonstructural protein NS2

Query Match 94.6%; Score 574; DB 2; Length 121;

Best Local Similarity 94.2%; Pred. No. 2.4e-42;

Matches 114; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MDPNTVSSFDILMRISKQMGSSSEDLNGIITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Db 1 MDPNTVSSFDILMRISKQMGSSSEDLNGMITQFESLKLYRDSLGAVMRMGDLHSLQN 60

Qy 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Db 61 RKGKWRQLGQKQFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPQL 120

Qy 121 I 121

Db 121 I 121

RESULT 10

MNIVXX

nonstructural protein NS2 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr

C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: A30086
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: D27846
A:Molecule type: genomic RNA
A:Residues: 1-118 <NAK>
A:CROSS-references: GB:M17070; NID:g324854; PIDN:AAA43549.1; PID:g324856
C:Genetics:
A:Gene: NS2
A:Map position: segment 8
A:Introns: 7/3
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.7%; Score 569; DB 1; Length 118;
Best Local Similarity 95.8%; Pred. No. 6.2e-42;
Matches 113; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 63
DB 1 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 60

QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121
DB 61 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 11
MNIV2
nonstructural protein NS2 - influenza A virus (strain A/PR/8/34)
C:Species: influenza A virus
C:Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 16-Jul-1999
C:Accession: A04096
R:Baez, M.; Taussig, R.; Zazra, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.
Nucleic Acids Res. 6, 5845-5858, 1980
A:Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and comparison with other influenza A virus NS genes.
A:Reference number: A93714; MUID:81124304; PMID:7465426
A:Accession: A04096
A:Molecule type: genomic RNA
A:Residues: 1-121 <BAE>
A:CROSS-references: GB:V01104; NID:g60803; PIDN:CAA24293.1; PID:g60805
C:Genetics:
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing

Query Match 93.4%; Score 567; DB 1; Length 121;
Best Local Similarity 93.4%; Pred. No. 9.4e-42;
Matches 113; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDNTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 60
DB 1 MDNTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 60

QY 61 RCKWTEQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 120
DB 61 RNEKWEQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 120

QY 121 I 121
DB 121 I 121

RESULT 12
MNIV4
nonstructural protein NS2 - influenza A virus (strain A/Duck/England/56 [H1N6]) (fragment)
C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: D27846

R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: D27846
A:Molecule type: genomic RNA
A:Residues: 1-118 <NAK>
A:CROSS-references: GB:M16563; NID:g324786; PIDN:AAA43511.1; PID:g324788
C:Genetics:
A:Gene: NS2
A:Map position: segment 8
A:Introns: 7/3
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 118;
Best Local Similarity 94.9%; Pred. No. 1.7e-41;
Matches 112; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 63
DB 1 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 60

QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121
DB 61 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 13
MNIV8
nonstructural protein NS2 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragment)
C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: H27846
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: H27846
A:Molecule type: genomic RNA
A:Residues: 1-118 <NAK>
A:CROSS-references: GB:M16565; NID:g324789; PIDN:AAA43513.1; PID:g324791
C:Genetics:
A:Gene: NS2
A:Map position: segment 8
A:Introns: 7/3
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 118;
Best Local Similarity 94.9%; Pred. No. 1.7e-41;
Matches 112; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 63
DB 1 NTVSSFDILMRISKMQLGSSSEDNGIITQFESLKYRDSLGEAVMRMGDLHSLQNRNG 60

QY 64 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 121
DB 61 KWREQLGQKFEIRWLIEVVRHRLKITENSFEQITFMQALQLLLEVEQIRTFSPOLI 118

RESULT 14
MNIVB4
nonstructural protein NS2 - influenza A virus (strain A/pintail/Alberta/119/79)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
C:Accession: H32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele, at the B locus of the NS gene.
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: H32662

A:Molecule type: genomic RNA
A:Residues: 1-121 <TR>
C:Genetics:
A:Gene: NS2
A:Map position: segment 8
A:Introns: 10/3
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.9%; Score 564; DB 1; Length 121;
Best Local Similarity 93.4%; Pred. No. 1.7e-41;
Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDPNTVSSFQDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVMRMGDLHSLQN 60
DB 1 MDSNTVSSFQDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVMRMGDLHSLQN 60
QY 61 RRGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQIRTFSPQL 120
DB 61 RRGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQIRTFSPQL 120
QY 121 I 121
DB 121 I 121

RESULT 15

nonstructural protein NS2 - influenza A virus (strains A/pintail/Alberta/268/78 and A/ma
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 19-Oct-1995
C:Accession: B32662; D32662
R:Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: B32662
A:Molecule type: genomic RNA
A:Residues: 1-121 <TR>
A:Experimental source: strain A/pintail/Alberta/268/78
A:Accession: D32662
A:Molecule type: genomic RNA
A:Residues: 1-121 <TR>
A:Experimental source: strain A/mallard/New York/6750/78
C:Genetics:
A:Gene: NS2
A:Map position: segment 8
A:Introns: 10/3
C:Superfamily: influenza virus nonstructural protein NS2
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 563; DB 1; Length 121;
Best Local Similarity 93.4%; Pred. No. 2.1e-41;
Matches 113; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDPNTVSSFQDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVMRMGDLHSLQN 60
DB 1 MDSNTVSSFQDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVMRMGDLHSLQN 60
QY 61 RRGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQIRTFSPQL 120
DB 61 RRGKWEQLGQKFEIRWLIEVVRHLKITENSFEQITFMQALQLLLEVEQIRTFSPQL 120
QY 121 I 121
DB 121 I 121

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OM protein - protein search, using sw model

Run on: September 22, 2005, 21:32:32 ; Search time 75.4957 Seconds
(without alignments)
820.730 Million cell updates/sec

Title: US-10-654-737-6

Perfect score: 607

Sequence: 1 MDPNTVSSFQDILMRISKMQ.....ALQLLLEVEQEIRTFSQLI 121

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	99.5	121	2 Q89733	Q89733 influenza a
2	600	98.8	121	2 Q67248	Q67248 influenza a
3	597	98.4	121	1 VNS2 IAUSS	P03504 influenza a
4	596	98.2	121	2 Q06049	Q06049 influenza a
5	594	97.9	121	1 VNS2 IAANN	P21432 influenza a
6	594	97.9	121	2 Q6XTJ1	Q6xtj1 influenza a
7	594	97.9	121	2 Q6XTJ7	Q6xtj7 influenza a
8	590	97.2	121	1 VNS2 IALB2	P26133 influenza a
9	590	97.2	121	2 Q67264	Q67264 influenza a
10	590	97.2	121	2 Q6XTI9	Q6xti9 influenza a
11	590	97.2	121	2 Q6XTK1	Q6xtk1 influenza a
12	589	97.0	121	2 Q8QIT5	Q8qit5 influenza a
13	589	97.0	121	2 Q6XTI5	Q6xti5 influenza a
14	589	97.0	121	2 Q6XTI7	Q6xti7 influenza a
15	588	96.9	121	1 VNS2 IAFOM	P03506 influenza a
16	587	96.7	121	1 VNS2 IACHI	P11619 influenza a
17	587	96.7	121	2 Q67255	Q67255 influenza a
18	587	96.7	121	2 Q6XTJ5	Q6xtj5 influenza a
19	587	96.7	121	2 Q771X1	Q771x1 influenza a
20	586	96.5	121	1 VNS2 IAFOW	P03505 influenza a
21	586	96.5	121	2 Q693C3	Q693c3 influenza a
22	586	96.5	121	2 Q6DQJ2	Q6dqj2 influenza a
23	586	96.5	121	2 Q6DSV1	Q6dsv1 influenza a
24	586	96.5	121	2 Q612B7	Q612b7 influenza a
25	586	96.5	121	2 Q6XTC3	Q6xtc3 influenza a
26	586	96.5	121	2 Q6XTF1	Q6xtf1 influenza a
27	586	96.5	121	2 Q6XTF3	Q6xtf3 influenza a
28	586	96.5	121	2 Q6XTF5	Q6xtf5 influenza a
29	586	96.5	121	2 Q6XTF7	Q6xtf7 influenza a
30	586	96.5	121	2 Q6XTF9	Q6xtf9 influenza a
31	586	96.5	121	2 Q6XTG1	Q6xtg1 influenza a

32	586	96.5	121	2 Q6XTG3	Q6xtg3 influenza a
33	586	96.5	121	2 Q6XTG5	Q6xtg5 influenza a
34	586	96.5	121	2 Q6XTG9	Q6xtg9 influenza a
35	586	96.5	121	2 Q6XTH1	Q6xth1 influenza a
36	586	96.5	121	2 Q6XTH7	Q6xth7 influenza a
37	586	96.5	121	2 Q6XTH9	Q6xth9 influenza a
38	586	96.5	121	2 Q6XTI1	Q6xti1 influenza a
39	586	96.5	121	2 Q77AL4	Q77al4 influenza a
40	585	96.4	121	2 Q8QLS0	Q8qls0 influenza a
41	584	96.2	121	2 Q41648	Q41648 influenza a
42	584	96.2	121	2 Q6XTJ3	Q6xtj3 influenza a
43	584	96.2	121	2 Q6XTJ9	Q6xtj9 influenza a
44	583	96.0	121	1 VNS2 IAPI0	P13148 influenza a
45	583	96.0	121	2 Q6XTG7	Q6xtg7 influenza a

ALIGNMENTS

RESULT 1

Q89733 ID Q89733 PRELIMINARY; PRT; 121 AA.
AC Q89733;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Non-structural protein 2.
GN Names=NS2;
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/WS/33; TISSUE=Embryonated;
RA Husak P.J.;
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert Wood Johnson Medical School.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A/WSN/40; TISSUE=Mouse;
RA Husak P.J., Schlesinger R.W.;
RT "Replication of neurovirulent and non-neurovirulent human H1N1 influenza A viruses in mouse brain and nerve cell cultures: virus strain-specific and host cell-dependent variations in progeny virus asse.";
RL Thesis (1994), Molecular Genetics and Microbiology, U.M.D.N.J.-Robert Wood Johnson Medical School.
DR EMBL; U13683; AAA21583.1; -;
DR EMBL; U13682; AAA21581.1; -;
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; 1.
SQ SEQUENCE 121 AA; 14327 MW; B15C14C594F55922 CRC64;

Query Match 99.5%; Score 604; DB 2; Length 121;

Best Local Similarity 99.2%; Pred. No. 5.7e-44;

Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDPNTVSSFQDILMRISKMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN	60
Db	1	MDPNTVSSFQDILMRISKMGSSSEDLNGIITQFESLKYRDSLGEAVNRMGDLHSLQN	60
Qy	61	RNGKVRQEQGQKFEIRWLIEVRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSQL	120
Db	61	RNGKVRQEQGQKFEIRWLIEVRHLKKTENSFEQITFMQALQLLLEVEQEIRTFSQL	120
Qy	121	I 121	
Db	121	I 121	

RESULT 2

Q67248


```
AC P21432;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Nonstructural protein NS2.
GN Name=8;
OS Influenza A virus (strain A/Ann Arbor/6/60), and
OS Influenza A virus (strain A/Leningrad/134/57 H2N2).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OC NCBI_TaxID=135322, 128148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Ann Arbor/6/60; PubMed=2974219;
RX MEDLINE=89073759;
RA Cox N.J., Kitame F., Kendal A.P., Maassab H.F., Naevae C.;
RT "Identification of sequence changes in the cold-adapted, live
RT attenuated influenza vaccine strain, A/Ann Arbor/6/60 (H2N2).";
RL Virology 167:554-567(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Leningrad/134/57;
RX MEDLINE=92124758; PubMed=1733114;
RA Klimov A.I., Cox N.J., Yotov W.V., Rocha E., Alexandrova G.I.,
RA Kendal A.P.;
RT "Sequence changes in the live attenuated, cold-adapted variants of
RT influenza A/Leningrad/134/57 (H2N2) virus.";
RL Virology 186:795-797(1992).
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P21432-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P21431-1, P26131-1;
CC Sequence=External;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; M23968; AAA43552.1; -
DR EMBL; M81572; AAA19198.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; 1.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match          97.9%; Score 594; DB 1; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RKGKWEQLGQKFEIRWLIEEVRHKLKITEVSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 I 121
DB 121 I 121

RESULT 6
Q6XTJ1 PRELIMINARY; PRT; 121 AA.
ID Q6XTJ1
AC Q6XTJ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Malaya/16/58 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=220954;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210153; AAC46572.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; 1.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match          97.9%; Score 594; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RKGKWEQLGQKFEIRWLIEEVRHKLKITEVSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 I 121
DB 121 I 121

RESULT 8
Q6XTJ1 PRELIMINARY; PRT; 121 AA.
ID Q6XTJ1
AC Q6XTJ1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Malaya/16/58 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=220954;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210156; AAC46578.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; 1.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match          97.9%; Score 594; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RKGKWEQLGQKFEIRWLIEEVRHKLKITEVSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 I 121
DB 121 I 121

RESULT 7
Q6XTJ7 PRELIMINARY; PRT; 121 AA.
ID Q6XTJ7
AC Q6XTJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Davis/1/57 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OC NCBI_TaxID=220951;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E., Cox N.J., Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210153; AAC46572.1; -
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00601; Flu_NS2; 1.
SQ SEQUENCE 121 AA; 14351 MW; DB9C1097D2D12584 CRC64;

Query Match          97.9%; Score 594; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 4.1e-43;
Matches 117; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRISKMLGSSSEDNGIITQFESLKYRDSLGEAVNRMGDLHSLQN 60
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RKGKWEQLGQKFEIRWLIEEVRHKLKITEVSFEQITFMQALQLLLEVEQEIRTFSQL 120
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 I 121
DB 121 I 121

RESULT 8
VNS2_1ALE2
```

RP	SEQUENCE FROM N.A.
RX	MEDLINE=91272515; PubMed=2053297;
RA	Schultz U., Fitch W.M., Ludwig S., Mandler J., Scholtissek C.;
RT	"Evolution of pig influenza viruses.";
RL	Virology 183:61-73(1991).
DR	EMBL; M55484; AAA43498.1; -;
DR	GO; GO:0019012; C:virion; IEA.
DR	GO; GO:0003723; P:RNA binding; IEA.
DR	InterPro; IPR000256; Flu_NS1.
DR	InterPro; IPR000968; Flu_NS2.
DR	Pfam; PF00600; Flu_NS1; I.
DR	Pfam; PF00601; Flu_NS2; 1.
KW	Nonstructural protein.
SQ	SEQUENCE 121 AA; 14349 MW; F472E29D7D471C6F CRC64;
Query Match	97.2%; Score 590; DB 2; Length 121;
Best Local Similarity	96.7%; Pred. No. 9e-43;
Matches 116; Conservative	3; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MDNTVSSFDIILMRISKMLGSSSEDNLNGIIITQFESIKLYRDSLGEAVMRMGDLHSLQN 60
Dd	1 MDSNTVSSFDIILMRISKMLGSSSEDNLNGMITQFESIKLYRDSLGEALMRMGDLHSLQN 60
Qy	61 RKGKWRQLGQKFEEIRLWLIEEVHRHLKITENSFEQITFMQALLLEVEOEIRTFSQ 120
Dd	61 RKGKWRQLGQKFEEIRLWLIEEVHRHLKITENSFEQITFMQALLLEVEOEIRTFSQ 120
Qy	121 I 121
Dd	121 I 121
RESULT 10	
Q6XTI9	PRELIMINARY; PRT; 121 AA.
ID Q6XTI9	
AC Q6XTI9	
DT 03-JUL-2004	(TEMBLrel. 27, Created)
DT 05-JUL-2004	(TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004	(TEMBLrel. 27, Last annotation update)
DE	Non-structural protein NS2.
OC	Influenza A virus (A/albany/6/58 (H2N2)).
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC	Influenzavirus A; H2N2 subtype.
OX	NCBI_TaxID=220953;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Lindstrom S.E., Cox N.J., Klimov A.;
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY210157; AAC46580.1; -;
DR	InterPro; IPR000968; Flu_NS2.
DR	Pfam; PF00601; Flu_NS2; I.
SQ	SEQUENCE 121 AA; 14350 MW; DB9CID2C64DC9E32 CRC64;
Query Match	97.2%; Score 590; DB 2; Length 121;
Best Local Similarity	95.9%; Pred. No. 9e-43;
Matches 116; Conservative	4; Mismatches 1; Indels 0; Gaps 0;
Qy	1 MDNTVSSFDIILMRISKMLGSSSEDNLNGIIITQFESIKLYRDSLGEAVMRMGDLHSLQN 60
Dd	1 MDNTVSSFDIILMRISKMLGSSSEDNLNGMITQFESIKLYRDSLGEAVMRMGDLHSLQN 60
Qy	61 RKGKWRQLGQKFEEIRLWLIEEVHRHLKITENSFEQITFMQALLLEVEOEIRTFSQ 120
Dd	61 RKGKWRQLGQKFEEIRLWLIEEVHRHLKITENSFEQITFMQALLLEVEOEIRTFSQ 120
Qy	121 I 121
Dd	121 I 121
RESULT 11	
Q6XTK1	PRELIMINARY; PRT; 121 AA.
ID Q6XTK1	

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AC Q6XTK1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (strain A/Singapore/1/57 H2N2).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220949;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210151; AAC4568.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14381 MW; DB8C0196C2C02484 CRC64;

Query Match 97.0%; Score 590; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 9e-43; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

QY 61 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 1 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 12
Q8QLT5 PRELIMINARY; PRT; 121 AA.
AC Q8QLT5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Non structural protein 2.
GN Name=NS2;
OS Influenza A virus (A/Swine/Cote d'Armor/3633/84 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OX NCBI_TaxID=164041;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A/swine/Cotes d'Armor/3633/84;
RX MEDLINE=21904432; PubMed=11907321;
RA Marozin S.; Gregory V.; Cameron K.; Bennett M.; Valette M.; Aymard M.;
RA Ponl E.; Barigazzi G.; Lin Y.; Hay A.;
RT "Antigenic and genetic diversity among swine influenza A H1N1 and H1N2 viruses in Europe.";
RL J. Gen. Virol. 83:735-745 (2002).
DR EMBL; AJ344025; CAC86628.1; -.
DR GO; GO:0003723; rRNA binding; IEA.
DR InterPro; IPR0002566; Flu_NS1.
DR InterPro; IPR000968; Flu_NS2.
DR Pfam; PF00600; Flu NS1; 1.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14330 MW; 149A445351AD7865 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 1.1e-42; Mismatches 1; Indels 0; Gaps 0;
Matches 117; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDSNTVSSFDILMRISKVQLGSSSKDLNGIITQFESLKYRDSLGEALRMGDLHSLQN 60

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QY 61 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 61 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 13
Q6XTI5 PRELIMINARY; PRT; 121 AA.
AC Q6XTI5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/SaoPaolo/3/59 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210159; AAC46584.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14339 MW; CB721B67D2D12584 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.1e-42; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60
DB 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

QY 61 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120
DB 61 RKGKREQLGQKFEIRWLIEVRHLKLTENSFEQITFMQALQLLLEVEQIRTFSQL 120

QY 121 I 121
DB 121 I 121

RESULT 14
Q6XTI7 PRELIMINARY; PRT; 121 AA.
AC Q6XTI7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Non-structural protein NS2.
OS Influenza A virus (A/Victoria/15681/59 (H2N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H2N2 subtype.
OX NCBI_TaxID=220956;
RN [1]
RP SEQUENCE FROM N.A.
RA Lindstrom S.E.; Cox N.J.; Klimov A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY210159; AAC46582.1; -.
DR InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
SQ SEQUENCE 121 AA; 14339 MW; CB721B67D2D12584 CRC64;

Query Match 97.0%; Score 589; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.1e-42; Mismatches 2; Indels 0; Gaps 0;
Matches 116; Conservative 3;

QY 1 MDPNTVSSFDILMRISKVQLGSSSEDLNGIITQFESLKYRDSLGEAVRMGDLHSLQN 60

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Db 1 MDPNTVSSFDILMRASKMQLGSSSEDLNGMITQFESLKYRDSLGEAVVRMGDLHSLON 60
QY 61 RRGKWEQLGQKFEIRWLIEEVRRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPOL 120
Db 61 RRGKWEQLGQKFEIRWLIEEVRRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPOL 120

QY 121 I 121
Db 121 I 121

RESULT 15
VNS2 IAFOM STANDARD; PRT; 121 AA.
AC P03506;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Nonstructural protein NS2.
GN Name=8;
OS Influenza A virus (strain A/Fort Monmouth/1/47 H1N1).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=229411;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83164298; PubMed=6834468;
RA Krystal M.; Buonagurio D.A.; Young J.F.; Palese P.;
RT "Sequential mutations in the NS genes of influenza virus field strains.";
RL J. Virol. 45:547-554(1983).
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=NS2;
CC IsoId=P03506-1; Sequence=Displayed;
CC Name=NS1;
CC IsoId=P03499-1; Sequence=External;
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; K00576; AAA3524.1; -;
InterPro; IPR000968; Flu NS2.
DR Pfam; PF00601; Flu NS2; 1.
KW Alternative splicing; Nonstructural protein.
SQ SEQUENCE 121 AA; 14300 MW; ED67C64D21C9BE9F CRC64;

Query Match 96.9%; Score 588; DB 1; Length 121;
Best Local Similarity 95.9%; Pred. No. 1.3e-42;
Matches 116; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDPNTVSSFDILMRASKMQLGSSSEDLNGITQFESLKYRDSLGEAVVRMGDLHSLON 60
Db 1 MDPNTVSSFDILMRASKMQLGSSSEDLNGVITLFESLKYRDSLGEAVVRMGDLHSLON 60
QY 61 RRGKWEQLGQKFEIRWLIEEVRRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPOL 120
Db 61 RRGKWEQLGQKFEIRWLIEEVRRHLKITENSFEQITFMQALQLLLEVEQEIRTFSPOL 120
QY 121 I 121
Db 121 I 121